

Fig. 1

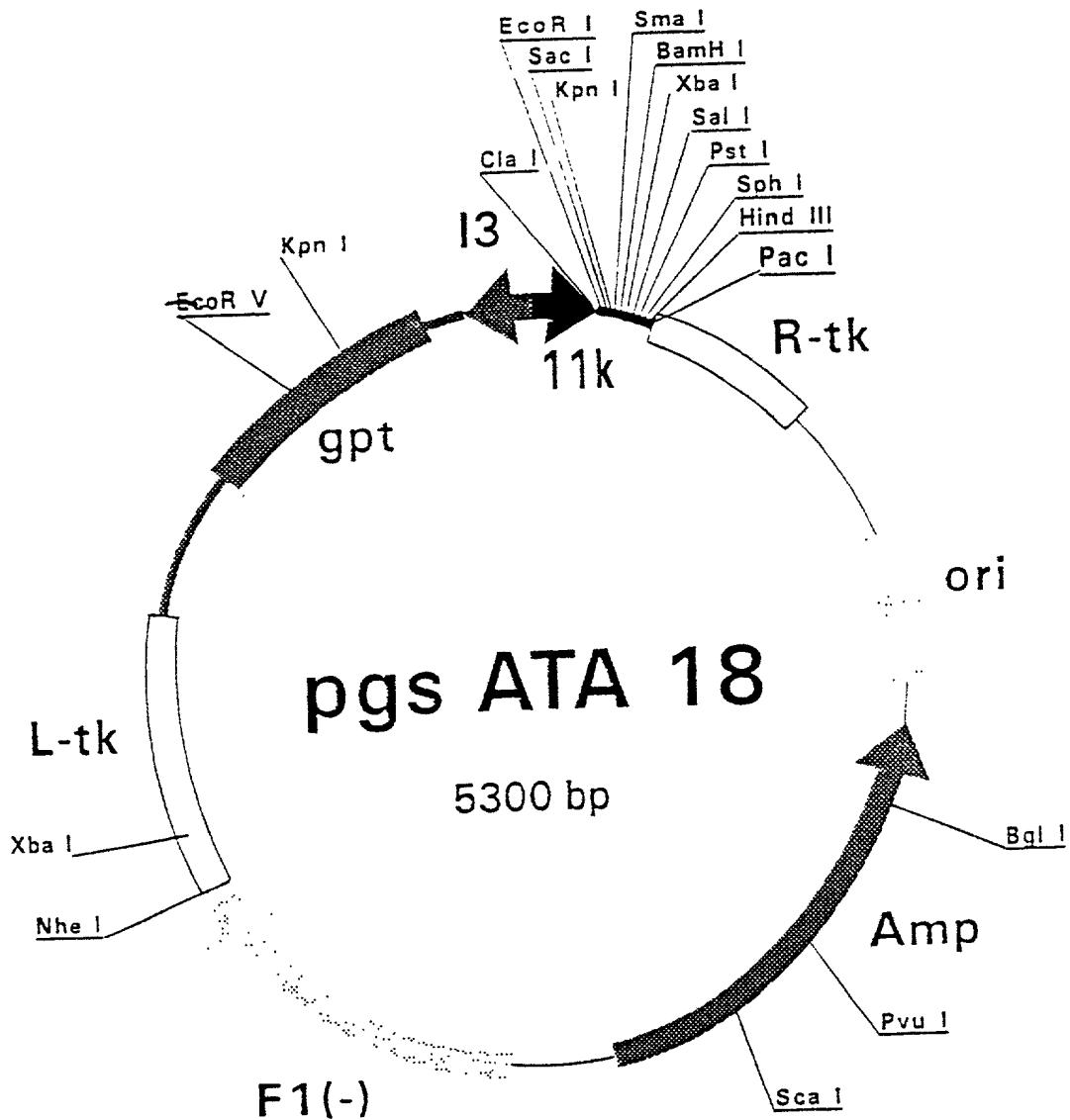


Fig. 2

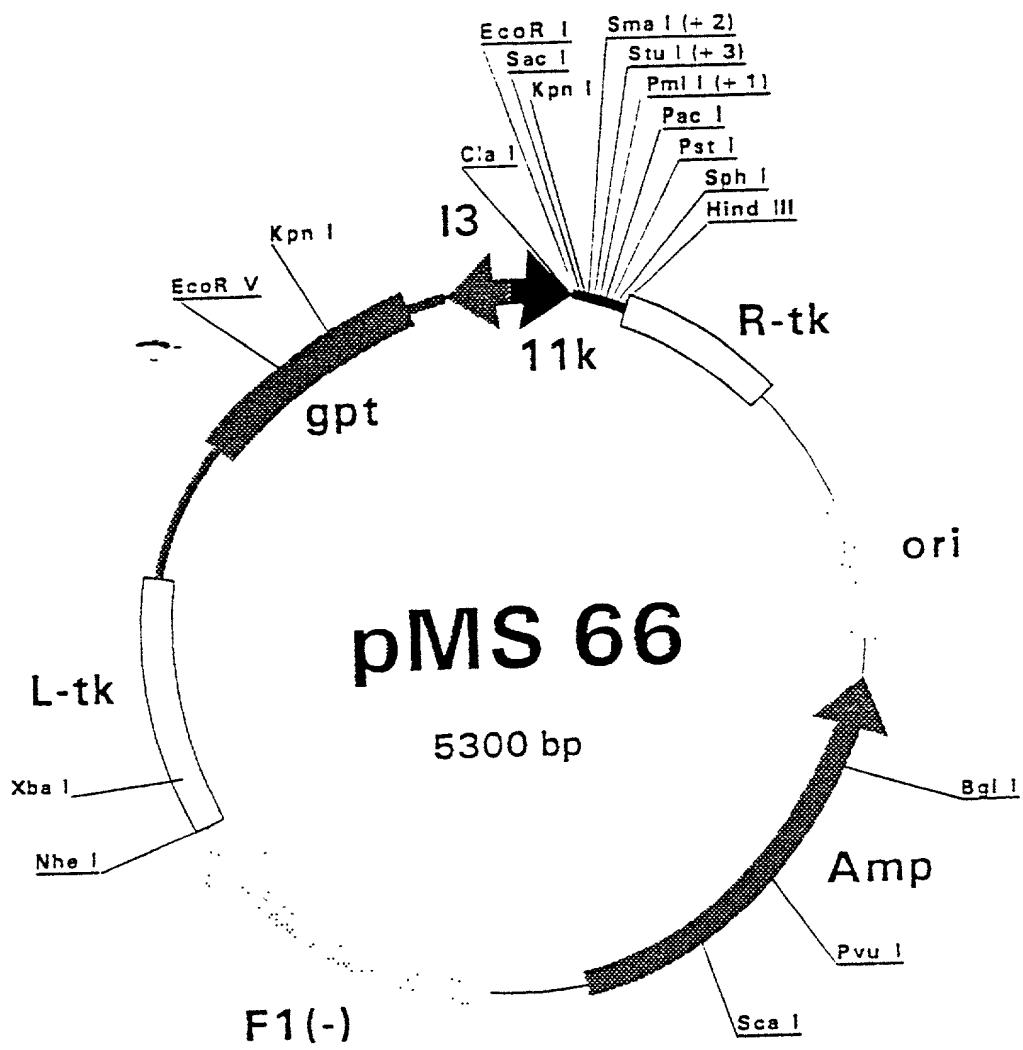


Fig. 3

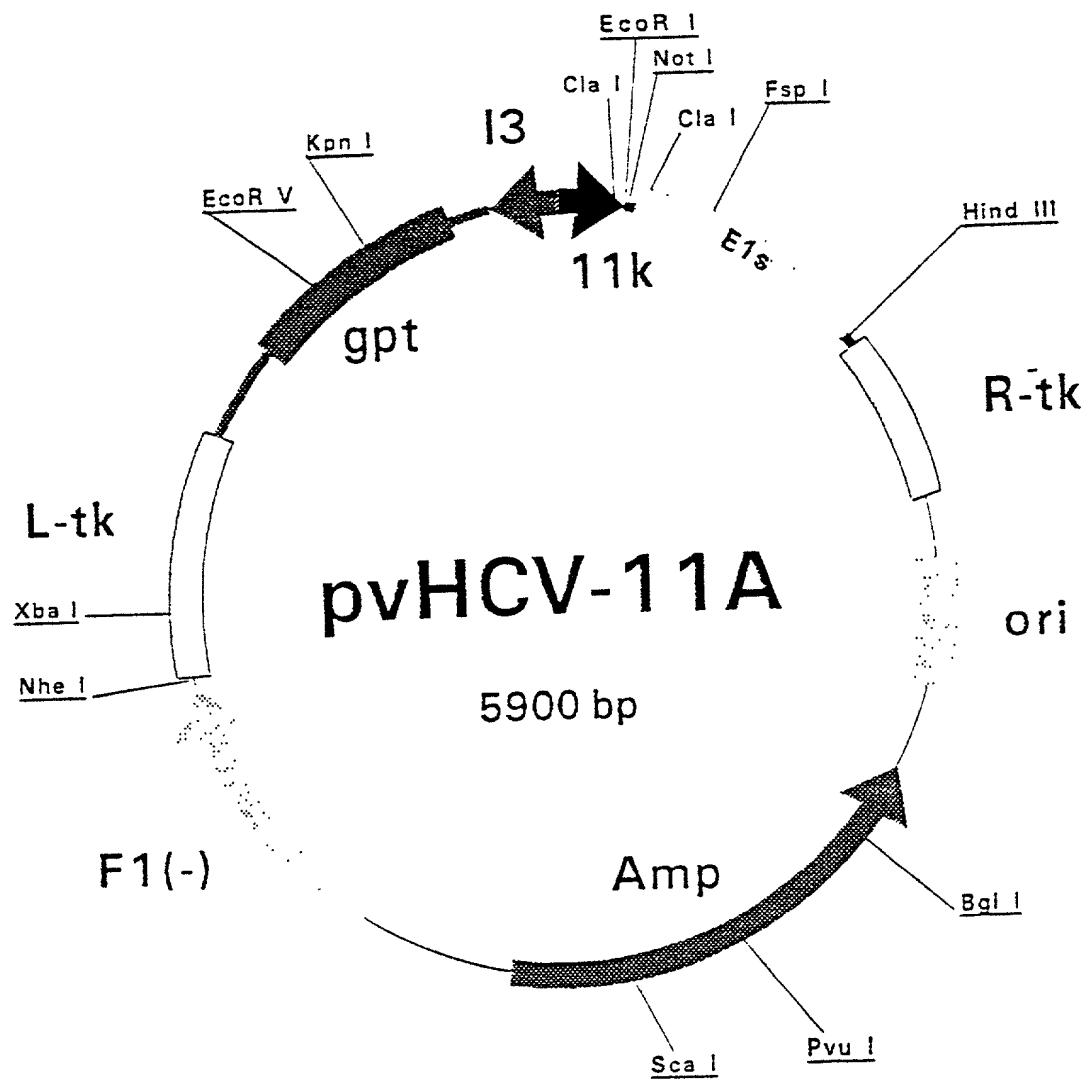
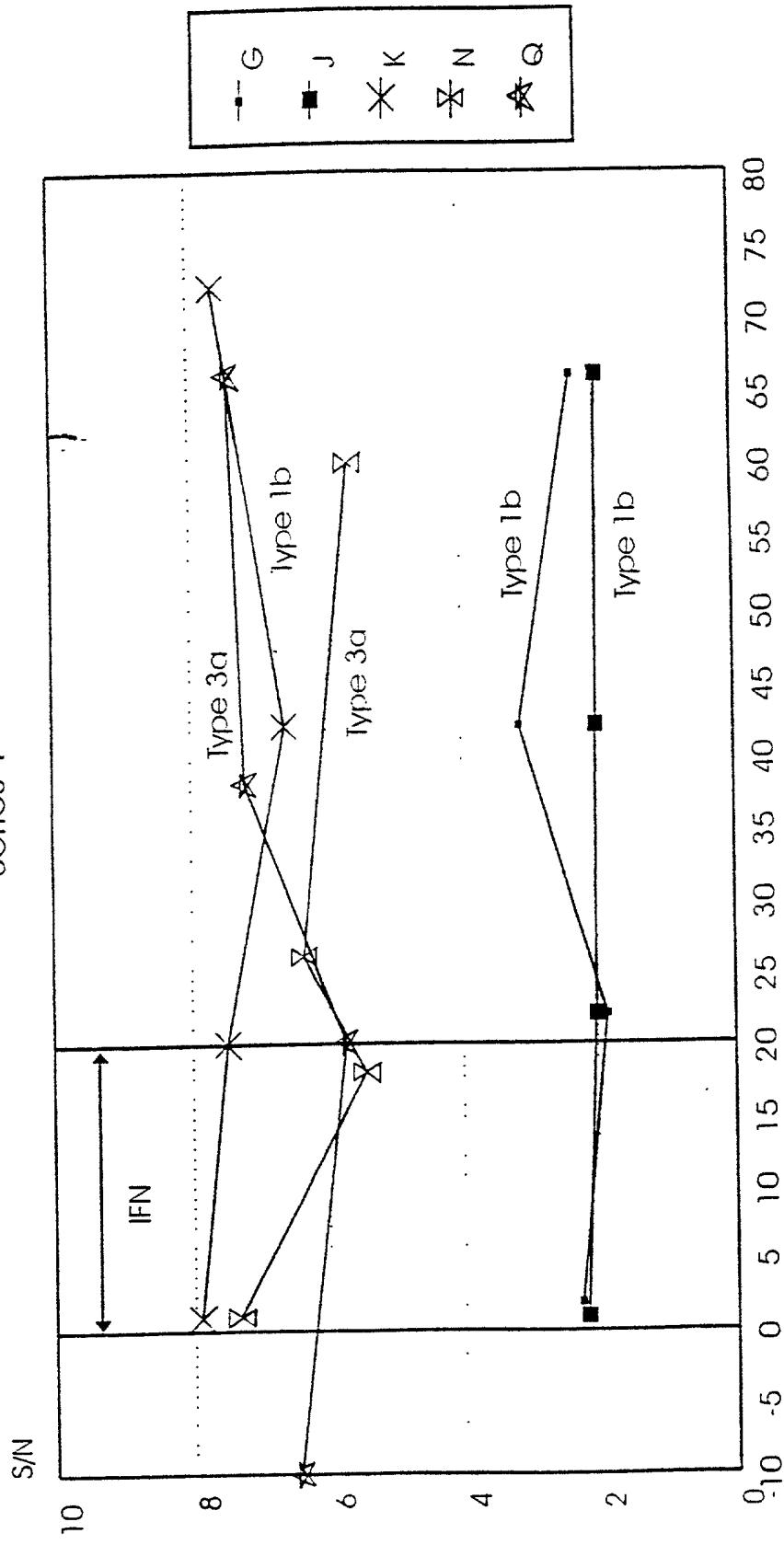


Fig. 4

Anti-E1 levels in NON-responders to IFN treatment

Series 1

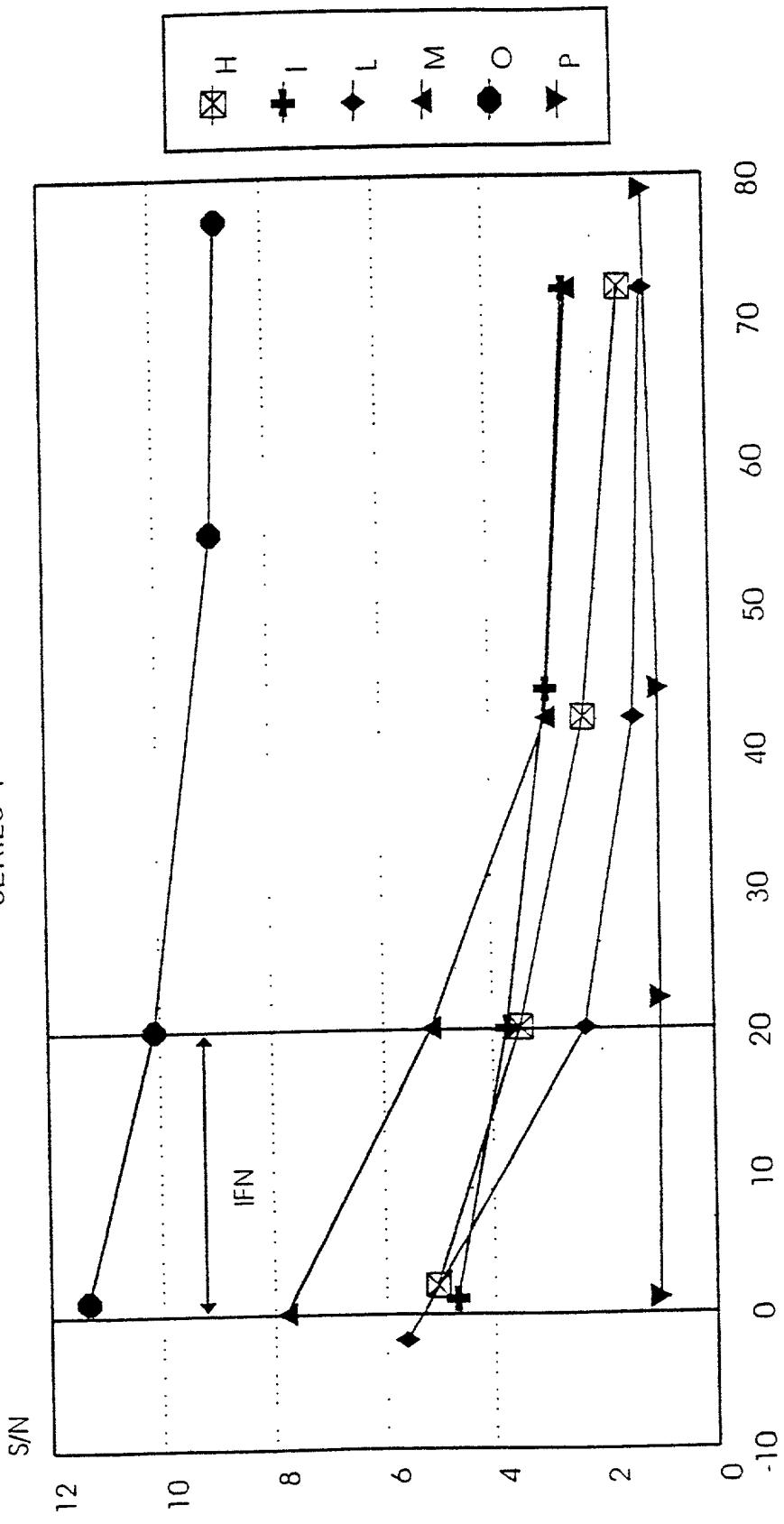


weeks after start of treatment

Fig. 5

Anti-E1 levels in RESPONDERS to IFN treatment

SERIES 1



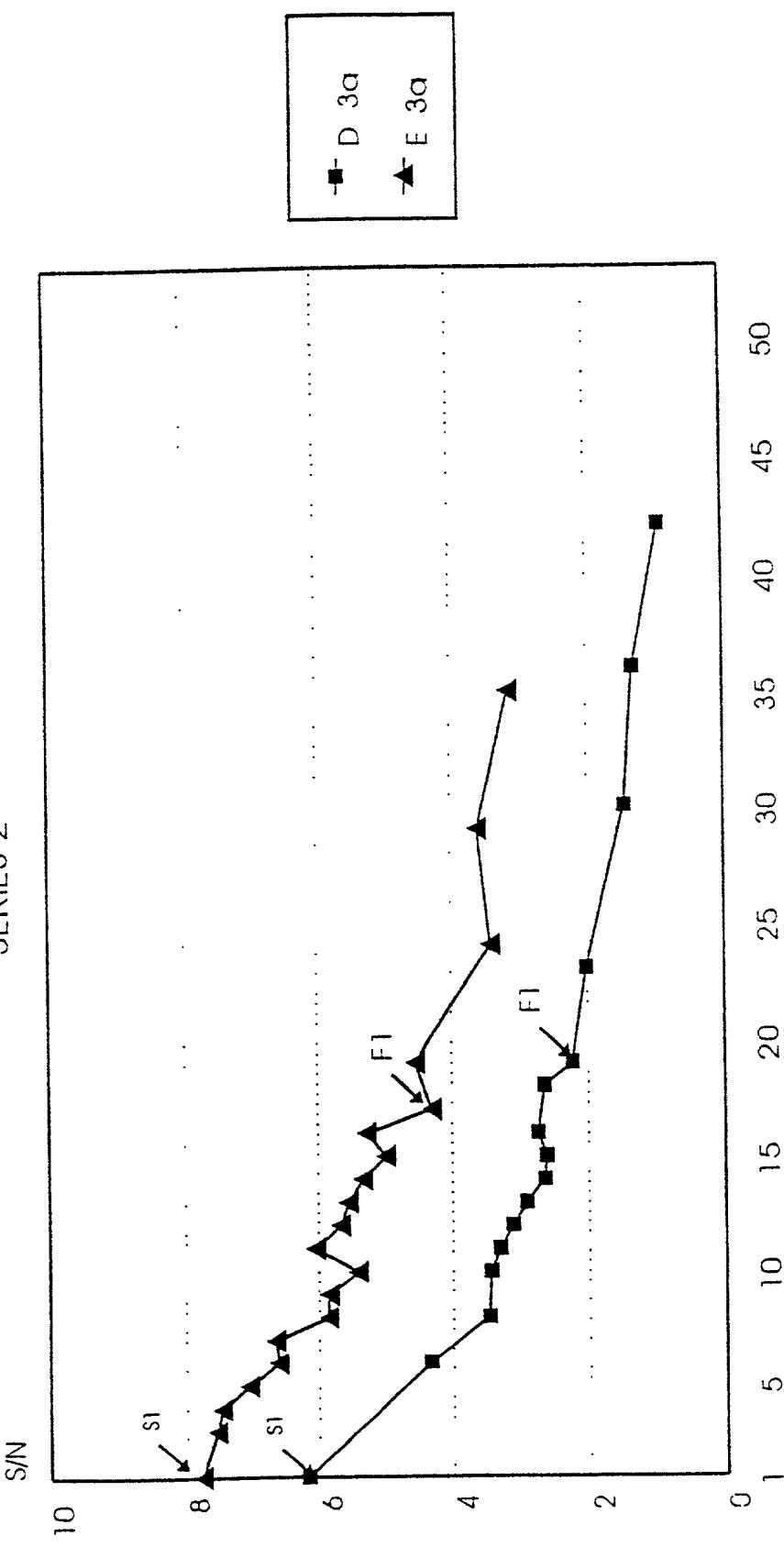
weeks after start of treatment

Fig. 6

Fig. 7. Anti-E1 levels in patients with COMPLETE response to IFN

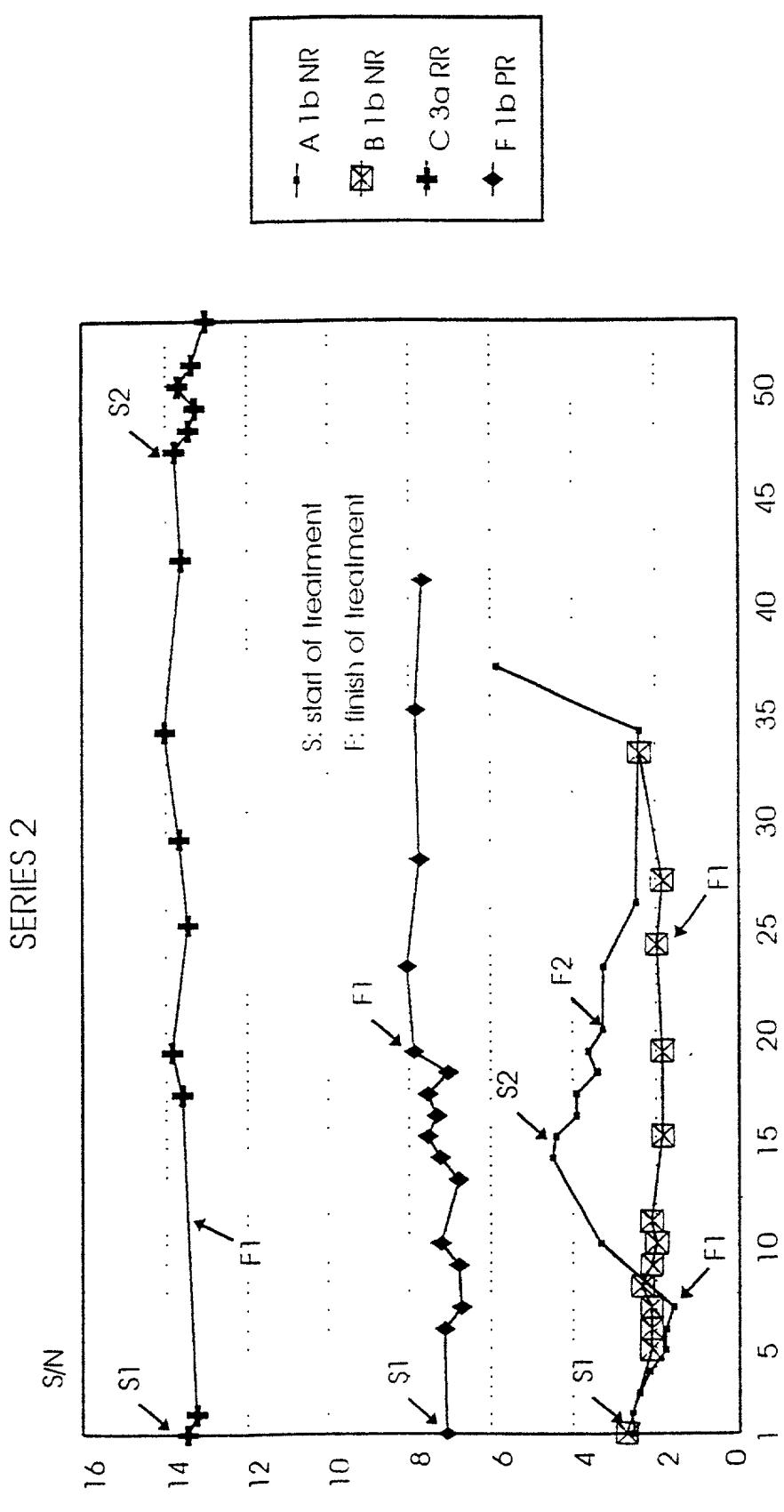
Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2



months after start of treatment
Fig. 7

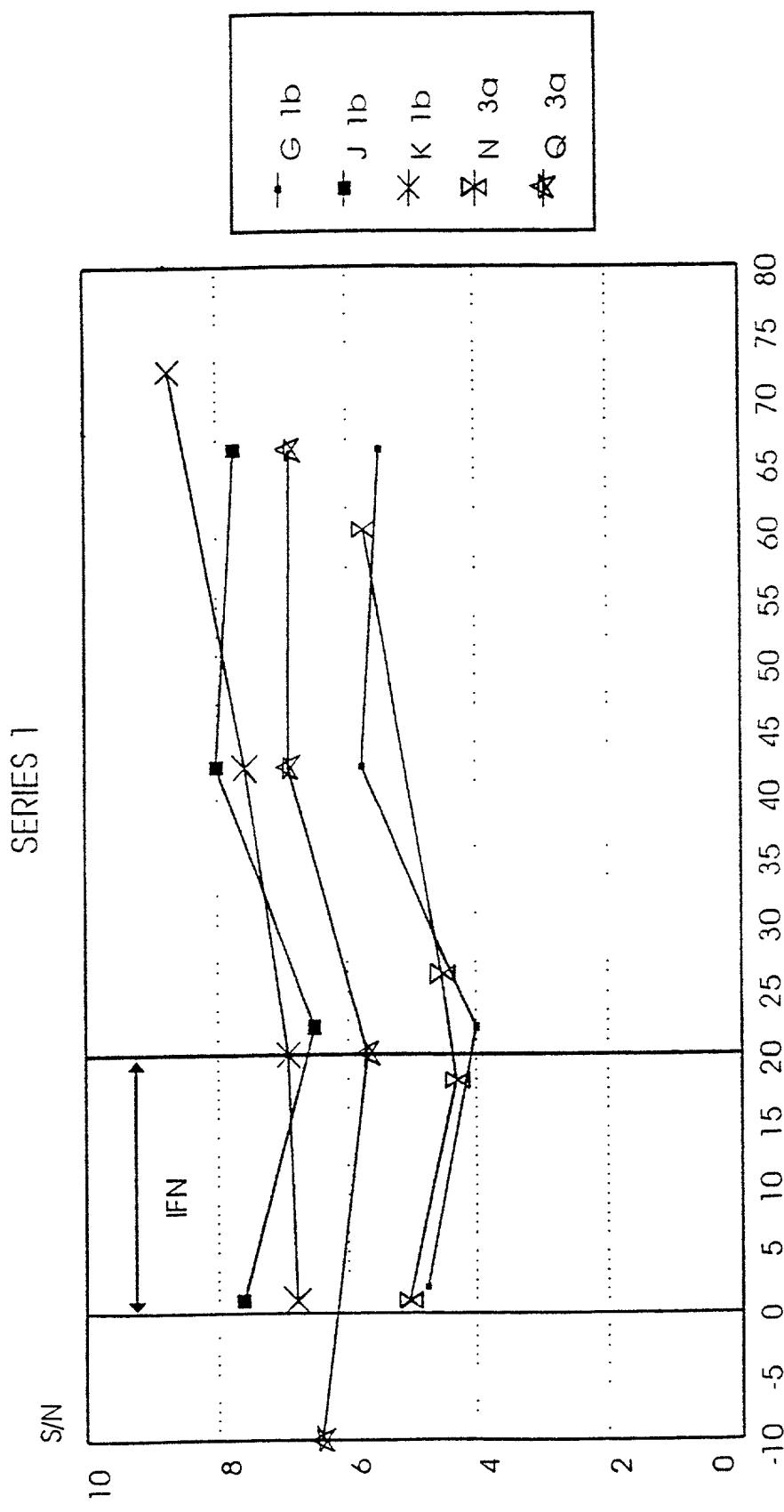
Anti-E1 levels in INCOMPLETE responders to IFN treatment



months after start of treatment

Fig. 8

Anti-E2 levels in NON-RESPONDERS to IFN treatment

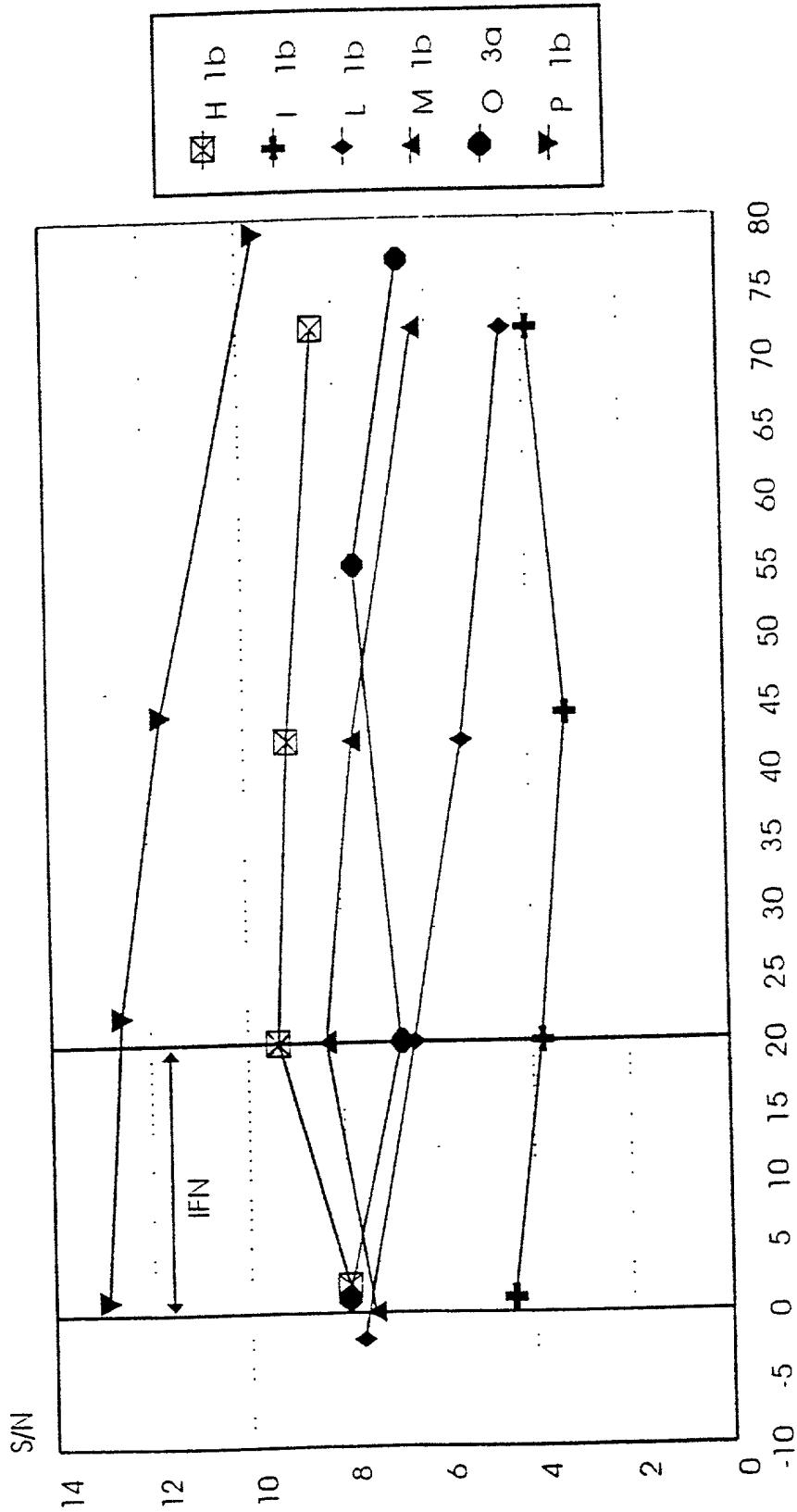


weeks after start of treatment

Fig. 9

Anti-E2 levels in RESPONDERS to IFN treatment

SERIES 1

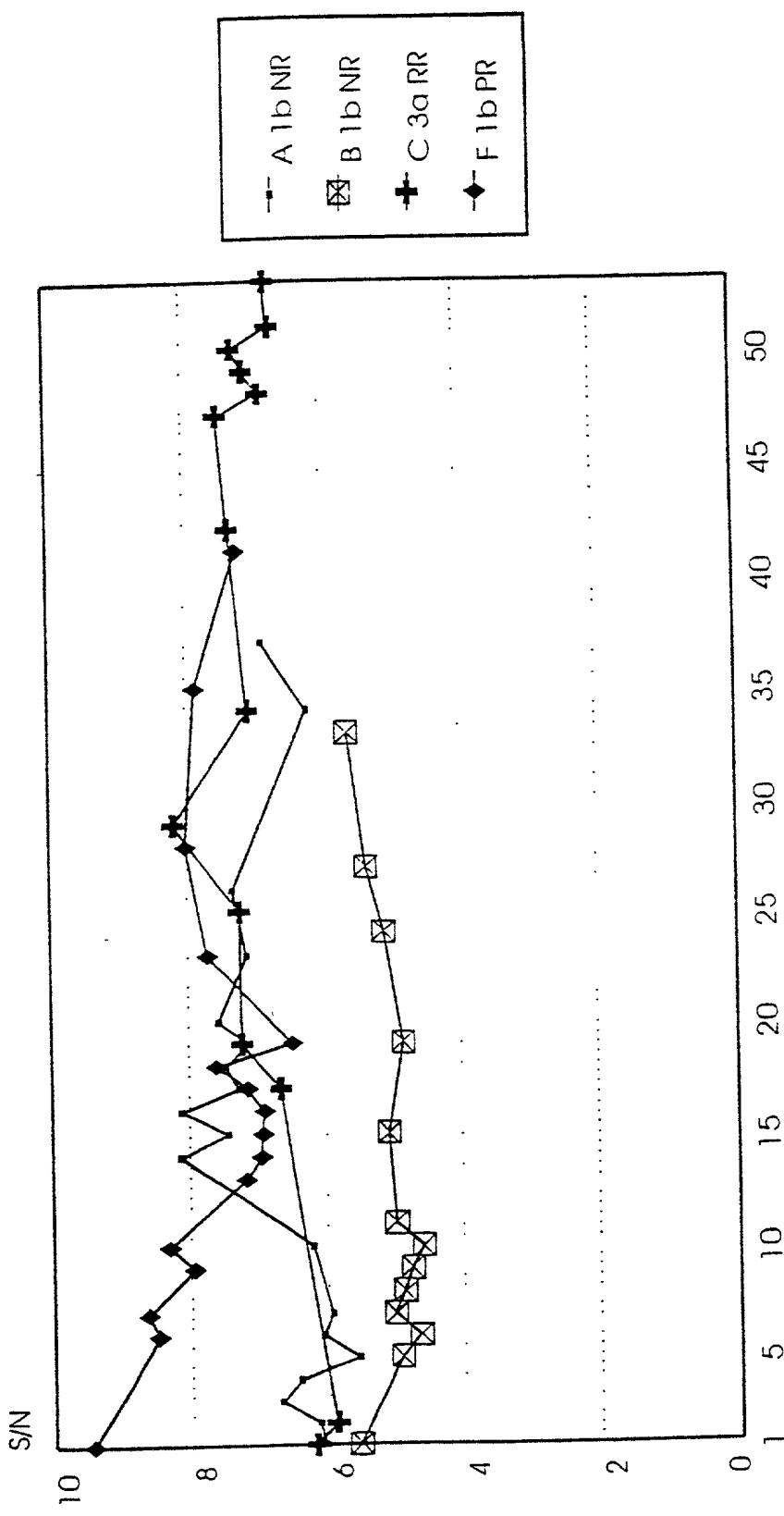


weeks after start of treatment

Fig. 10

Anti-E2 levels in INCOMPLETE responders to IFN treatment

SERIES 2

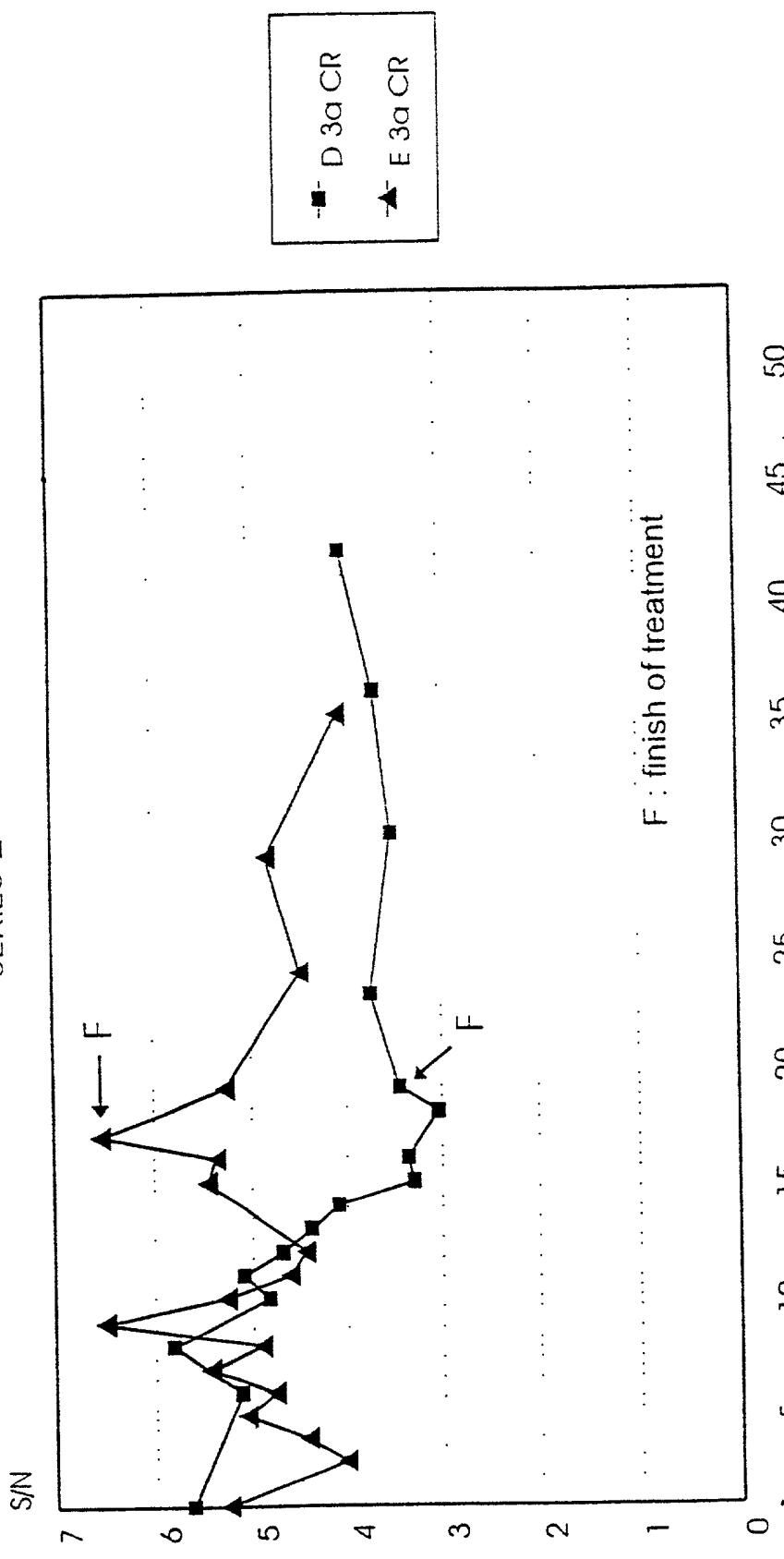


months after start of treatment

Fig. 11

Anti-E2 levels in COMPLETE responders to IFN treatment

SERIES 2



F : finish of treatment
months after start of treatment

Fig. 12

Human anti-E1 reactivity competed with peptides

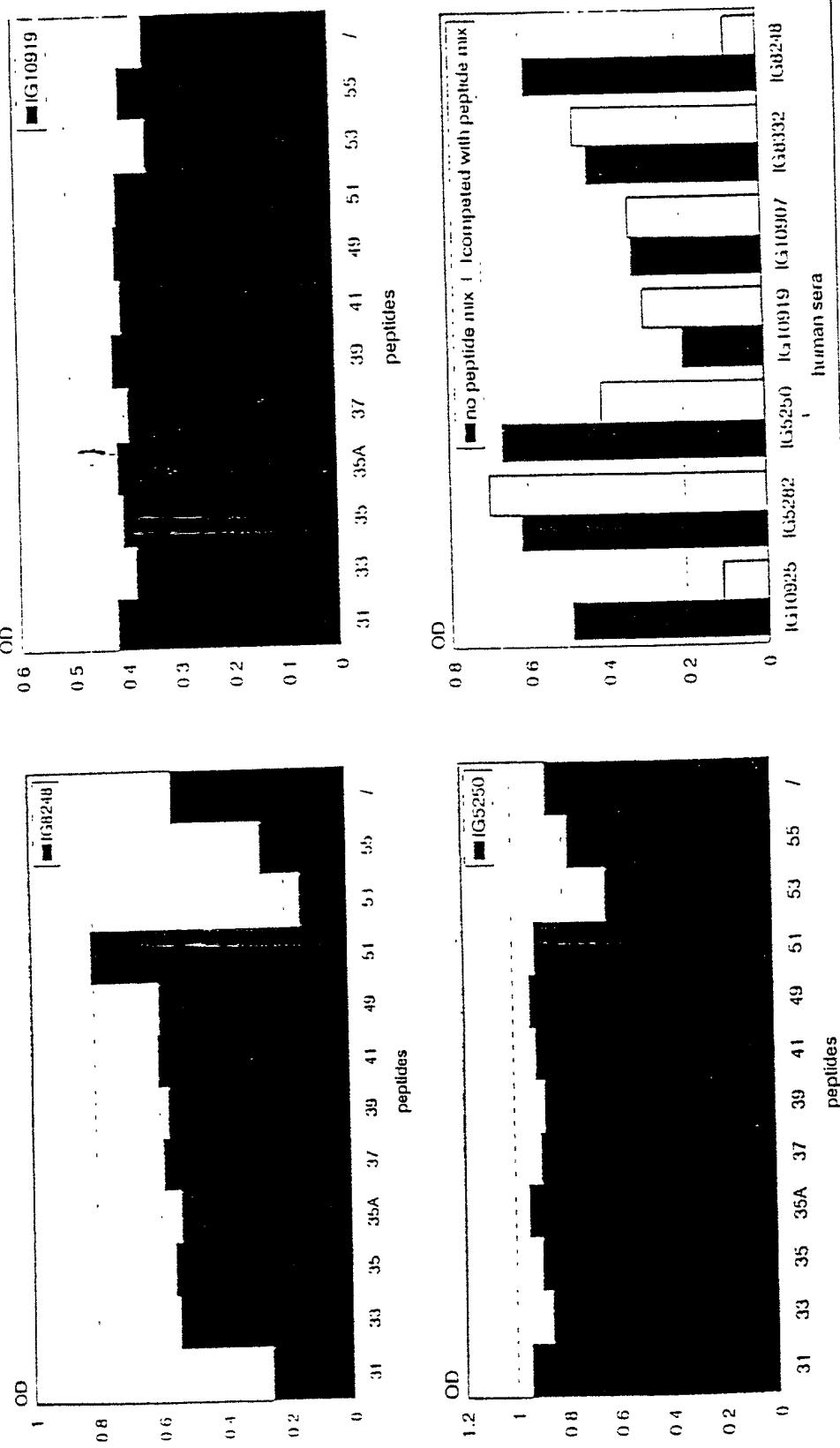


Fig. 13

Competition of reactivity of anti-E1 Mabs with peptides

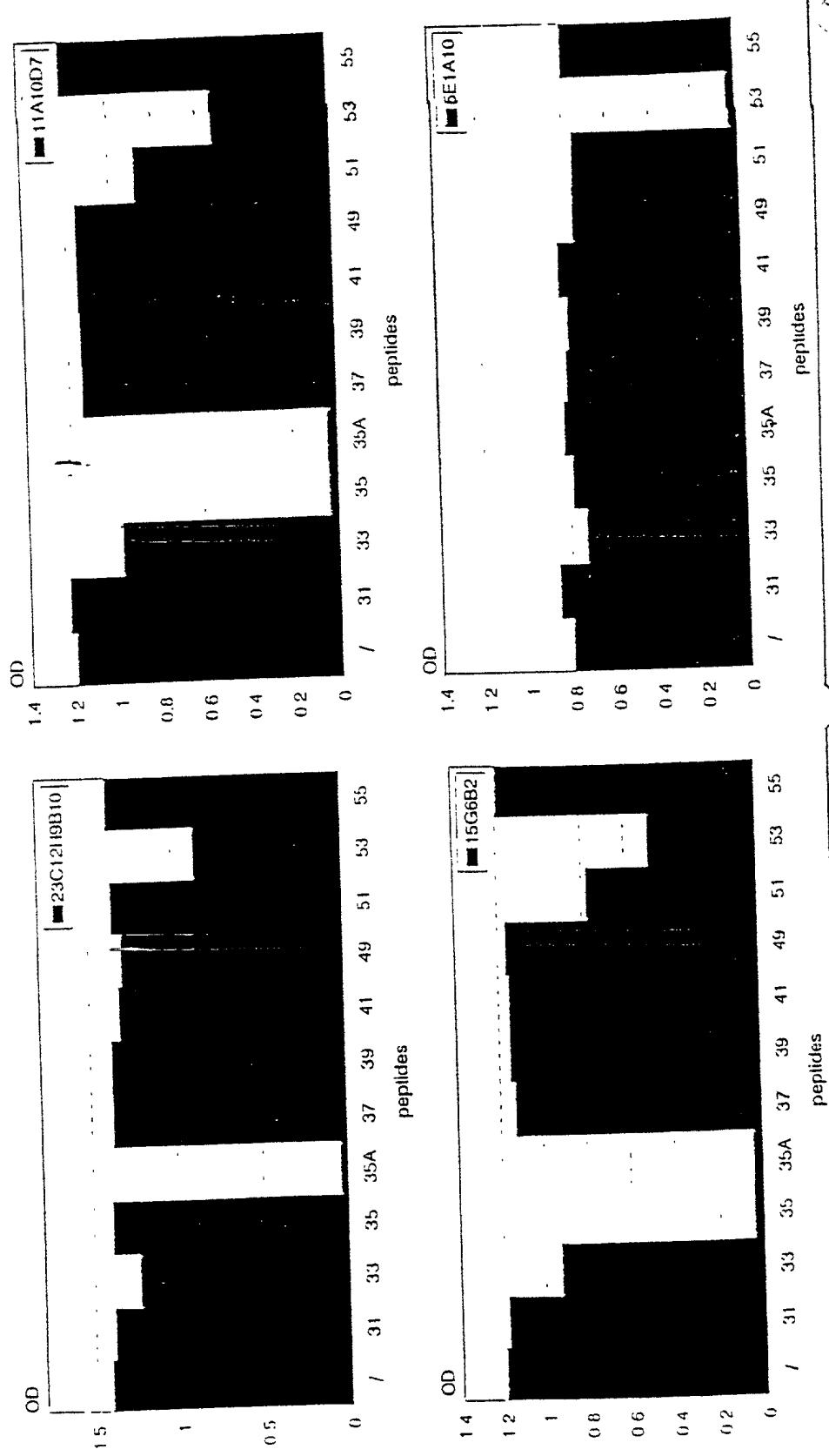
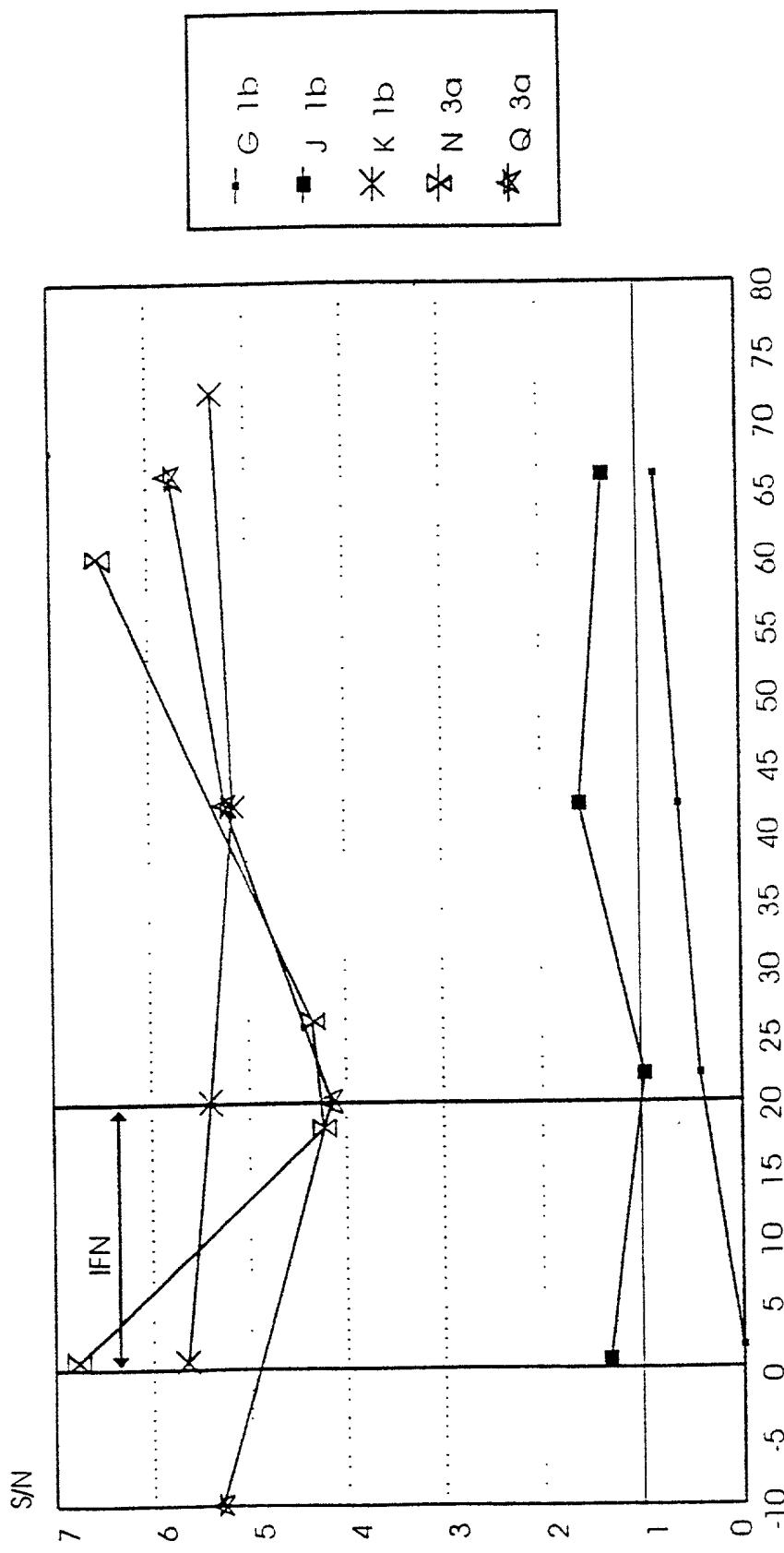


Fig.14

Anti-E1 (epitope 1) levels in NON-RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig. 15

Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment

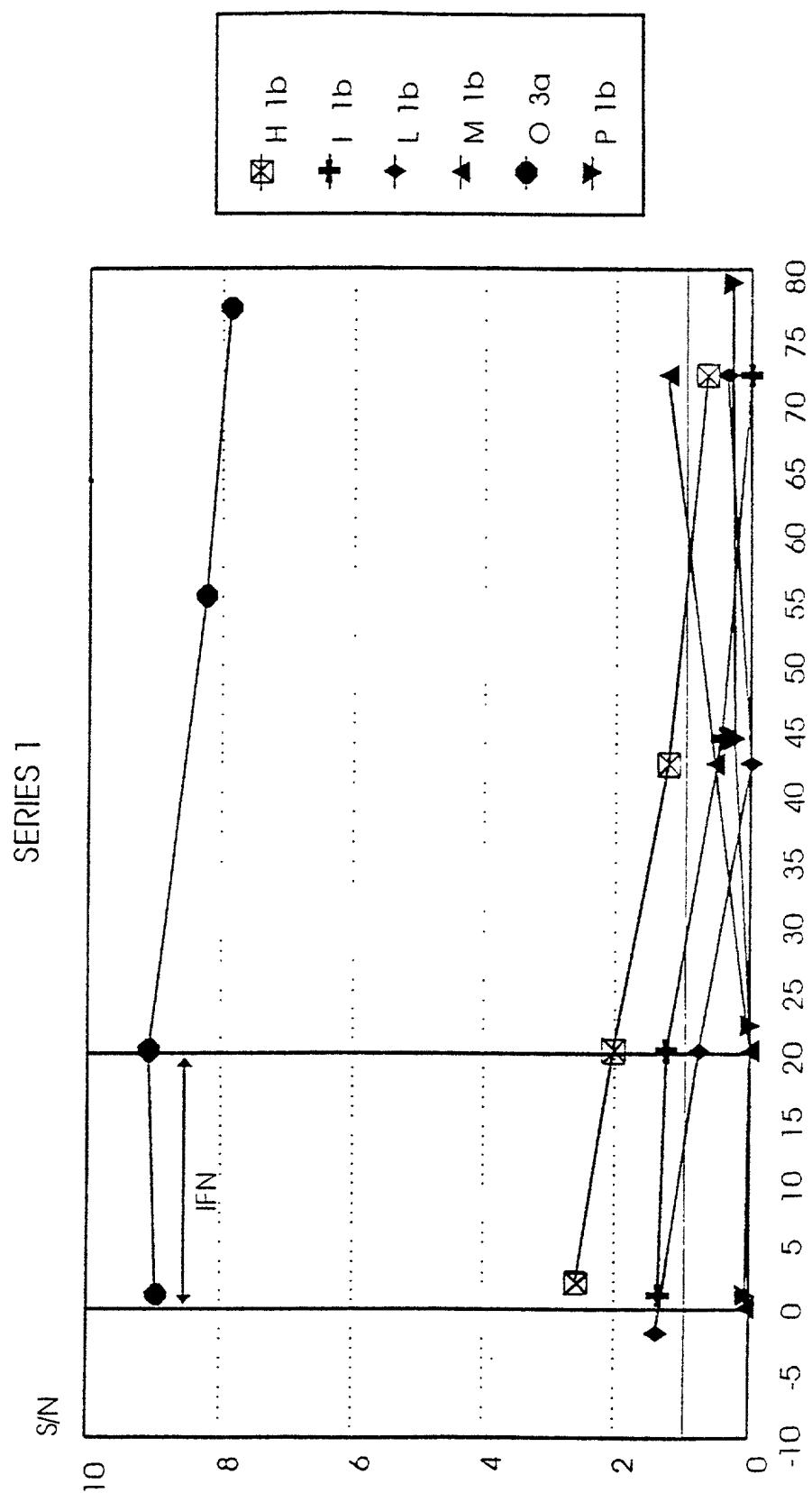
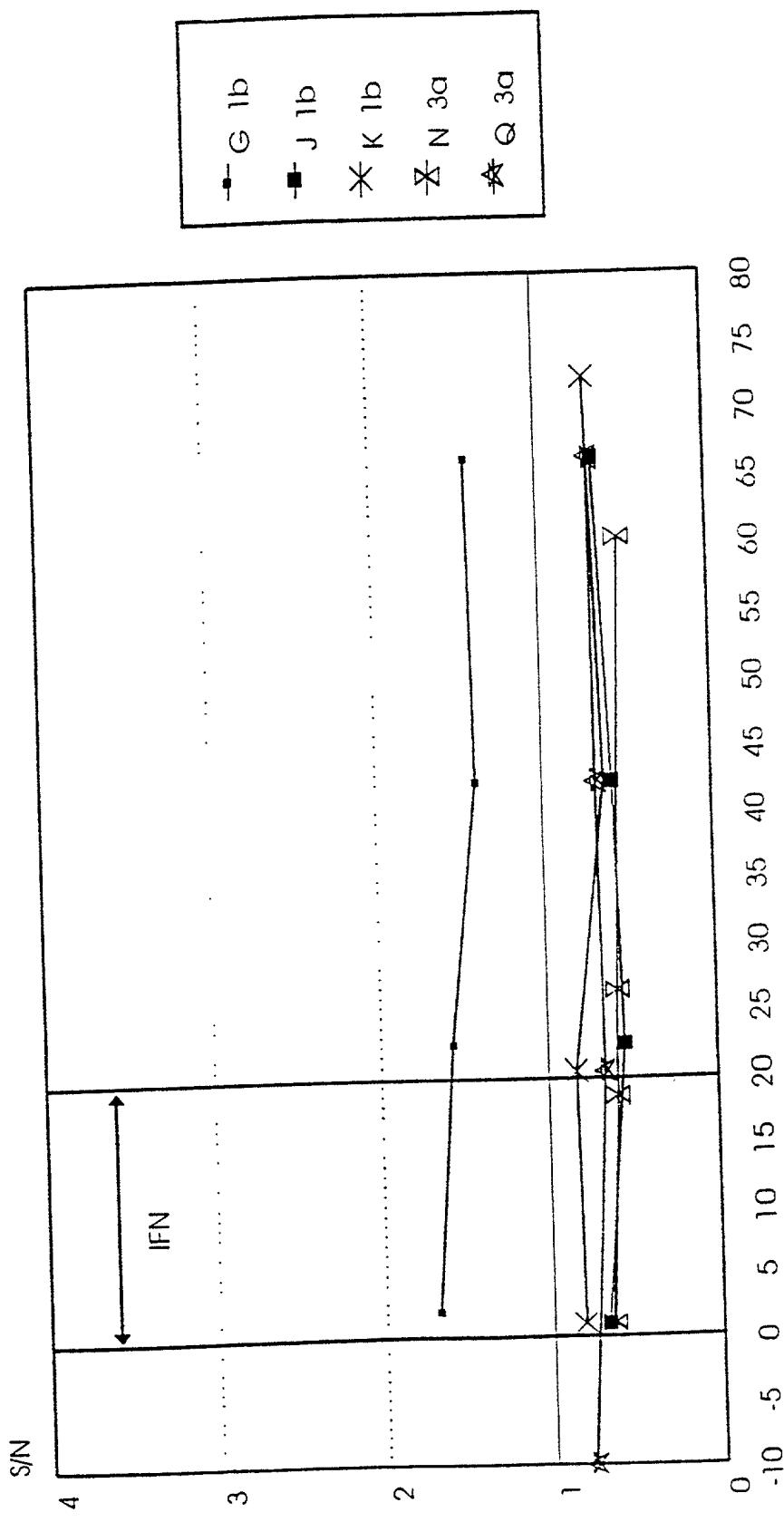


Fig. 16 weeks after start of treatment

Anti-E1 (epitope 2) levels in NON-RESPONDERS to IFN treatment

SERIES 1



weeks after start of treatment

Fig.17

Anti-E1 (epitope 2) levels in RESPONDERS to IFN treatment

SERIES 1

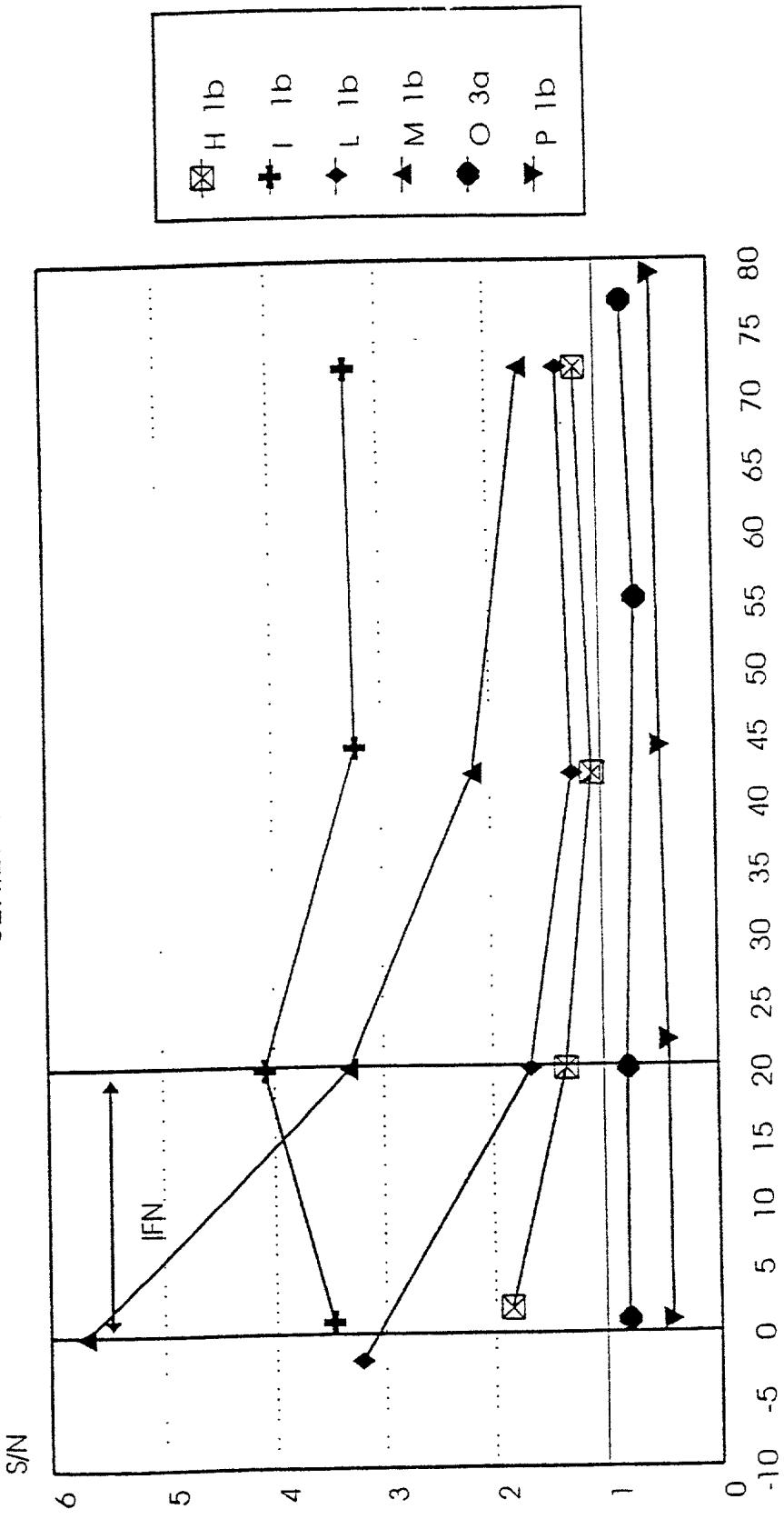


Fig.18
weeks after start of treatment

Competition of reactivity of anti-E2 Mabs with peptides

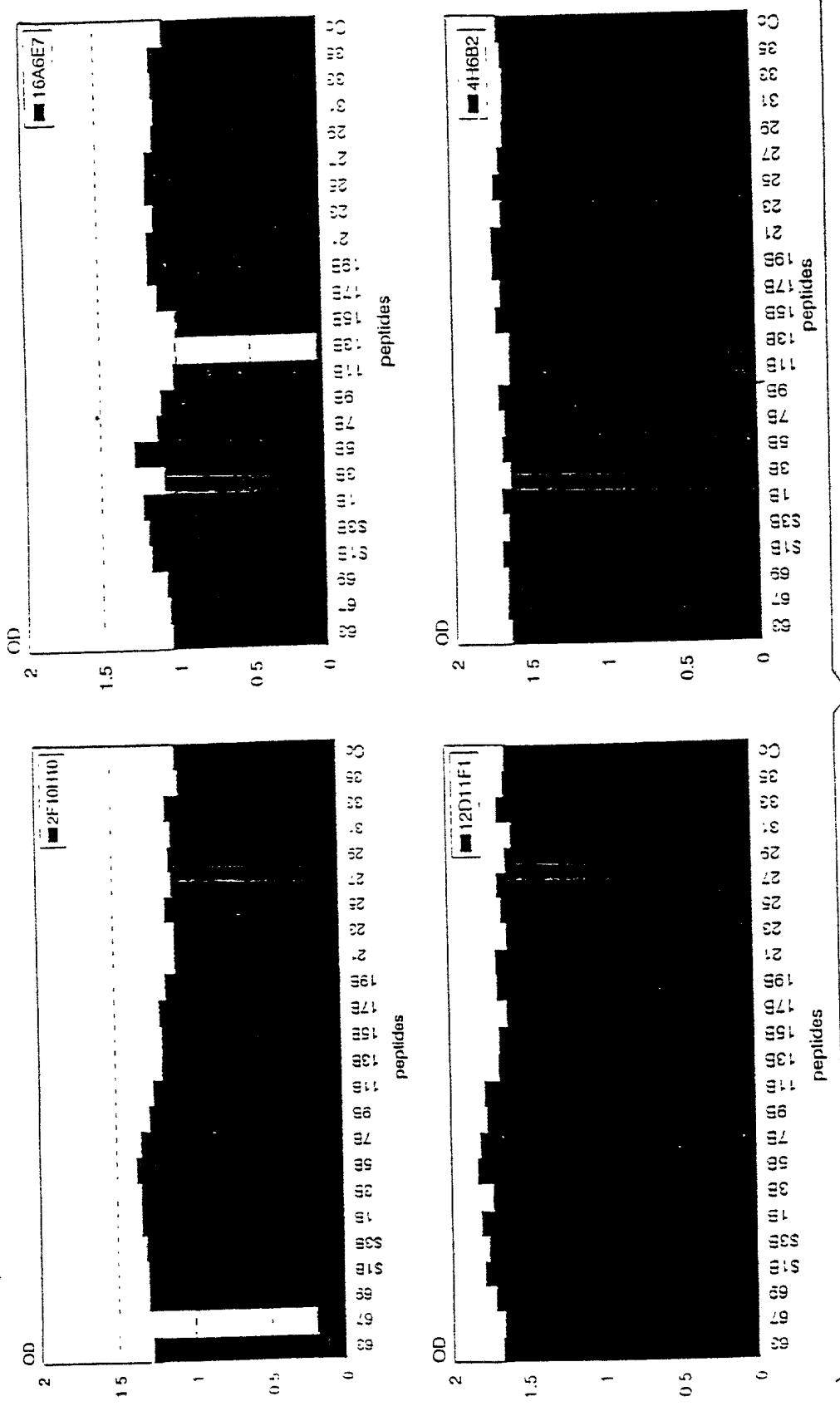


Fig. 19

Human anti-E2 reactivity competed with peptides

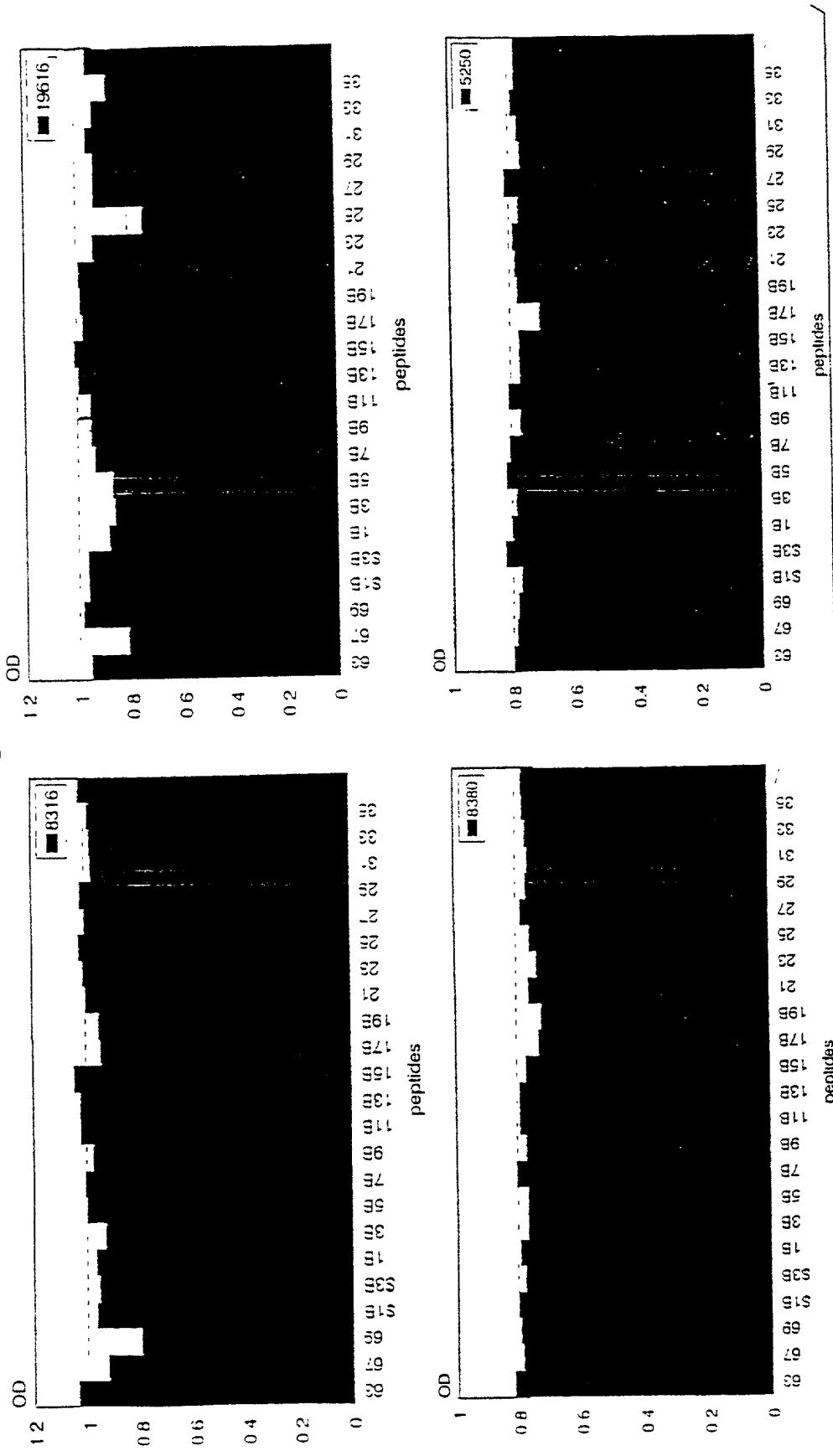


Fig. 20

Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)

3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

5'CCGGGGAGGCCTGCACGTGATCGAGGGCAGACACCATCACCAACCACACTAAATAGT
TAATTAACTGCA 3' (SEQ ID NO 2)

3'CCTCCGGACGTGCACTAGCTCCCGTCTGGTAGTGGTAGTATTATCAATTAATTG

5' (SEQ ID NO 95)

SEQ ID NO 3 (HCCI9A)

ATGCCCGGTTGCTCTTCTCTATCTTCCTCTGGCTTACTGTCCTGTCTGACCATTCCA
GCTTCCGCTTATGAGGTGCGAACGTGTCGGGATGTACCATGTCACGAACGACTGCT
CCAACCTCAAGCATTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGT
GCCCTGCGTTCGGGAGAACAACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTC
GCAGCTAGGAACGCCAGCGTCCCCACCACGACAATACGACGCCACGTCGATTGCTCG
TTGGGGCGGCTGCTCTGTTCCGCTATGTACGTGGGGATCTGCGGATCTGTCTTC
CTCGTCTCCAGCTGTTACCATCTCGCCTGCCGGCATGAGACGGTGAGGACTGCA
ATTGCTCAATCTATCCCGGCCACATAACAGGTACCGTATGGCTGGATATGATGAT
GAACTGGTCGCCTACAACGGCCCTGGTGTATCGCAGCTCCGGATCCCACAAGCT
GTCGTGGACATGGTGGCGGGGCCATTGGGAGTCCTGGCGGGCTCGCCTACTATT
CCATGGTGGGAACTGGCTAAGGTTTGATTGTGATGCTACTCTTGCTCTAATAG

SEQ ID NO 5 (HCCI10A)

ATGTTGGTAAGGTATCGATAACCTTACATGCGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGCGGCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGAAATTGCCGGTTGCTCTTCTCT
ATCTTCCCTTGGCTTGCTGCTGTACCGTTCCAGCTCCGCTTATGAAGTGCG
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACTAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGCCTGCGTTGGAGAAC
AACTCTTCCGCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACGACAATACGACGCCACGTCGATTGCTCGTTGGGGCGGCTGCTTCTG

Fig. 21B

TTCCGCTATGTACGTGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA
CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
CCACATAACGGGTACCGTATGGCTGGATATGATGATGAACCTGGTCGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG
GGGCCCATTGGGGAGTCCTGGCGGGTCTGCCTACTATTCCATGGTGGGGAACTGGGC
TAAGGTTTGATTGTGATGCTACTCTTGCTCCCTAATAG

SEQ ID NO 7 (HCCI11A)

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TTCCGCTCGTCGGCGCCCCCTAGGGGGTGCAGGCCAGAGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAACATGCAACAGGGATTGCTGGTTGCTCTTCTCTA
TCTTCCTCTGGCTTACTGTCTGTGACCATTCCAGCTTCCGCTTATGAGGTGCGC
AACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACTCAGCATTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTCGGGAGAAC
ACTCTTCCCGCTGCTGGTAGCGCTACCCCCACGCTCGAGCTAGGAACGCCAGCGT
CCCCACTACGACAATACGACGCCACGTCGATTGCTCGTGGGGCGGCTGCTTCTGTT
CCGCTATGTACGTGGGGATCTCTGCGATCTGCTTCCCTCGTCTCCAGCTGTTACCC
ATCTCGCCTGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG
ACATAACAGGTACCGTATGGCTGGATATGATGAACCTGGTAATAG

SEQ ID NO 9 (HCCI12A)

ATGCCCGGTTGCTCTTCTCTATCTTCCCTTGGCCCTGCTGTCTGTGACCATACCA
GCTTCCGCTTATGAAGTGCACGCGAACGTGTCCGGGTGTAACCATGTCACGAACGACTGCT
CCAACCTCAAGCATACTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGTGCCT
GCCCTGCCTCGGGAGGGCAACTCCTCCGTTGCTGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCACGCGTCCCCACAACGACAATACGACGCCACGTCGATTGCTC
GTTGGGGCTGCTGCTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTT
CCTTGTCTCCAGCTGTTCACCTCTCACCTGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTACCGCATGGCTGGATATGATGAT
GAACCTGGTCTTAATAG

SEQ ID NO 11 (HCCI13A)

ATGTCCGGTTGCTCTTCTCTATCTTCCCTTGGCCCTGCTGTCTGTGACCATACCA
GCTTCCGCTTATGAAGTGCACGCGAACGTGTCCGGGTGTAACCATGTCACGAACGACTGCT
CCAACCTCAAGCATACTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGTGCCT

Fig. 21C

GCCCTGCCTCGGGAGGGCAACTCCTCCCCTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATAACGACGCCACGTCGATTGCTC
GTTGGGGCTGCTGCTTCTGTTCCGCTATGTACGTGGGGATCTCTGCGGATCTGTTT
CCTTGTTCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCGGCCATGTATCAGGTACCCGCATGGCTGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

ATGCTGGGTAAAGGCCATCGATAACCCTAACGTGCGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAAGACGGCGTGAACATATGCAACAGGAATTGCTGGTTGCTCTTCTCTA
TCTTCCTCTGGCTTACTGTCTGTCTAACCAATTCCAGCTCCGCTTACGAGGTGCGC
AACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACACTAAGCATTGTATG
AGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCGTTGGGAGAAC
ACTCTTCCCCTGCTGGTAGCGCTACCCCCACGCTCGGGCTAGGAACGCCAGCAT
CCCCACTACAACAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTCTGTT
CCGCTATGTAACGTGGGGATCTCTGCGGATCTGTCTTCTCGTCTCCAGCTGTTACC
ATCTCGCCTCGCCGGCATGAGACGGTGCAAGGACTGCAATTGCTCAATCTATCCGGCC
ACATAACGGGTACCGTATGGCTGGATATGATGAACTGGTACTAATAG

SEQ ID NO 15 (HCPr51)

ATGCCCGGTTGCTCTTCTCTATCTT

SEQ ID NO 16 (HCPr52)

ATGTTGGTAAGGTACATCGATAACCCT

SEQ ID NO 17 (HCPr53)

CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)

CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)

ATACGACGCCACGTCGATTCCAGCTGTTACCCATC

Fig. 21D

SEQ ID NO 20 (HCPr108)

GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

ATGTTGGTAAGGTATCGATAACCCTTACATGCGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTCTGGAGGAACGGCGTGAACATGCAACAGGAAATTGCCCGTTGCTCTTCTCT
ATCTCCTCTTGGCTTGCTGTCTGACCGTTCCAGCTCCGCTTATGAAGTGCG
AACGTGTCGGGATGTACCATGTCACGAACGACTGCTCCAACCTAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTCGGGAGAAC
AACTCTTCCCCTGCTGGTAGCGCTCACGCTCGAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCATTGGGG
AGTCCTGGCGGGCTCGCCTACTATTCCATGGTGGGAACGGCTAAGGTTTGATTG
TGATGCTACTCTTGCTCCCTAATAG

SEQ ID NO 23 (HCCI38)

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TTCCGCTCGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTCTGGAGGAACGGCGTGAACATGCAACAGGAAATTGCCCGTTGCTCTTCTCT
ATCTCCTCTTGGCTTGCTGTCTGACCGTTCCAGCTCCGCTTATGAAGTGCG
AACGTGTCGGGATGTACCATGTCACGAACGACTGCTCCAACCTAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCCTGCCTCGGGAGAAC
AACTCTTCCCCTGCTGGTAGCGCTCACGCTCGAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTGGATATGATGATGAACTGGTAA
TAG

SEQ ID NO 25 (HCCI39)

ATGTTGGTAAGGTATCGATAACCCTTACATGCGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTCTGGAGGAACGGCGTGAACATGCAACAGGAAATTGCCCGTTGCTCTTCTCT

Fig. 21E

ATCTTCCTTTGGCTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTAT
GAGGCAGCGAACATGATCATGCACACCCCCGGTGCCTGCCCTGCAGTCGGGAGAAC
AACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCAGGCCACATAACGGG
CACCGTATGGCTGGGATATGATGATGAACGGTGCCTACAACGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTAATAG

SEQ ID NO 27 (HCCI40)

ATGTTGGTAAGGTATCGATAACCTTACATGGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGCGCCCGCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACATATGCAACAGGAATTGCCCCGGTTGCTCTTCT
ATCTTCCTTTGGCTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTCAAGCATTGTAT
GAGGCAGCGAACATGATCATGCACACCCCCGGTGCCTGCCCTGCAGTCGGGAGAAC
AACTCTTCCCCTGCTGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCAGGCCACATAACGGG
CACCGTATGGCTGGGATATGATGATGAACGGTGCCTACAACGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCGTGAAGGGCAGACACCACCACTAATAG

SEQ ID NO 29 (HCCI62)

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CGCTCGTCGGCGCTCCCGTAGGAGGCCTGCAAGAGGCCCTGCCATGGCGTGGGC
CCTTGAAGACGGATAAAATTGCAACAGGAATTGCCGGTTGCTCTTCTATT
TCCTTCTCGCTCTGTTCTTGTCTTAAATTCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCTTACCAACGACTGTTCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGGCAATACA
TCCACGTGCTGGACCCAGTGCACACCTACAGTGGCAGTCAAGTACGTGGAGCAACCA
CCGCTTGCATACGCACTGTTGGACCTATTAGTGGCGGGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGCTTCCCTGTTGGACAAGCCTTACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACGTGCTGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTGGGATATGATGATGAACGGTAAATAG

Fig. 21F

SEQ ID NO 31 (HCC163)

ATGGGTAAGGTACATCGATAACCTAACGTGCGGATTGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCAGCCCCATTGGGGCGTCGAAGGGCTCTGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGAATTACCCGGTTGCTCTTCTCTATCT
TTATTCTTGCTCTCTCGTGTGACCGTTCCGGCCTCTGCAGTCCCTACCGAAATG
CCTCTGGATTATCATGTTACCAATGATTGCCAAACTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCGGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACCGTGTGGGCACTATTCTGGTAGGCCAAATGTTCACCTATA
GGCCTCGCCAGCAGCCTACGGTCAGAACTGCAACTGTTCCATTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGATATGATGATGAACGGTAATAG

SEQ ID NO 33 (HCPr109)

TGGGATATGATGATGAACGGTC

SEQ ID NO 34 (HCPr72)

CTATTATGGTGGTAAKGCCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

TGGGATATGATGAACGGTCGCCTACAACGGCCCTGGTGGTATCGCAGCTGCTCC
GGATCCCACAAGCTGCGTGGACATGGTGGGGGGCCATTGGGGAGTCTGGCGG
GCCTCGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGGTGTATGCTACTC
TTGCCGGCGTCGACGGGATACCCGCGTGTCAAGGAGGGCAGCAGCCTCCGATAACCA
GGGGCCTTGTGTCCCTCTTAGCCCCGGTCGGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAAC TGCAACGACTCCCTCAAAC
AGGGTTCTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGCGCTCATCGACAAGTTGCTCAGGGTGGGTCCCTCACTT
ACACTGAGCTAACAGCTCGGACCAGAGGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCCGTCTCAGGTGTGGTCCAGTGATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGACCGACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAAACACGCGGCCGCCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGTTACCAAGACGTGTGGGGCCCCCGTGAACA
TCGGGGGGCCGGCAACAAACACCTTGACCTGCCCACTGACTGTTTGGGAAGCACCC
CGAGGCCACCTACGCCAGATGCGGTTCTGGCCCTGGCTGACACCTAGGTGTATGGTT

Fig. 21G

CATTACCCATATAAGGCTCTGGCACTACCCCTGCAGTCAACTTCACCATCTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCCTTGTGACTTGAGGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCCCTCACCAACCCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCTGTTGCTCTTCTCCT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGCCTCAATCGGGCGCCGTGGCCGGGCGATGGC
ACTCTTCCTCCTTGTGTTCTCTGTGCTGCTGGTACATCAAGGGCAGGCTGGTCCC
TGGTGCAGCATAACGCCCTATGGCGTGGCCGCTGCTCCTGCTTCTGCTGGCCTTAC
CACACAGAGCTTATGCCTAGTAA

SEQ ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCATTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGAACCTGGCTAAGGTTTGGTTGTGATGCTACTCT
TTGCCGGCGTCGACGGCATAACCGCGTGTCAAGGAGGGCAGCAGCCTCCGATACCA
GGGGCCTTGTGTCCTCTTACCCCCGGGTCGGCTCAGAAAATCCAGCTCGAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGCGCTCCATCGACAAGTTGCTCAGGGTGGGGTCCCTCACTT
ACACTGAGCTAACAGCTGGACCAGAGGCCACTGCTGGCACTACGCCCTCGACC
GTGTGGTATTGTACCCCGTCTCAGGTGTGCGGTCAGTGTATTGCTTACCCCCGAGCC
CTGTTGTGGGGGACGACCGATGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTAACAAACACGCCGCCGCCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGTTACCAAGACGTGTGGGGCCCCCGTGAACA
TCGGGGGGCCGGCAACAACACCTTGACCTGCCCCACTGACTGTTTCGGAAGCACC
CGAGGCCACCTACGCCAGATGGTTCTGGCCCTGGCTGACACCTAGGTGTATGGTT
CATTACCCATATAAGGCTCTGGCACTACCCCTGCAGTCAACTTCACCATCTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTGAAGCCGCATGCAATTGGACTCG
AGGAGAGCCTTGTGACTTGAGGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGAGTGGCAGAGCTTAATTAAATTAG

SEQ ID NO 39 (HCCI42)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCATTGGGGAGTCCTGGCGGG
CCTCGCCTACTATTCCATGGTGGGAACCTGGCTAAGGTTTGGTTGTGATGCTACTCT

Fig. 21H

TTGCCGGCGTCGACGGGCATAACCGCGTGTCAAGGAGGGCAGCAGCCTCCGATACCA,
GGGGCCTTGTGTCCCTCTTAGCCCCGGGCGCTCAGAAAATCCAGCTCGTAAACAC
CAACGGCAGTTGGCACATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAAC
AGGGTTCTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAG
CGCTTGGCCAGCTGCGCTCCATCGACAAGTTCGCTCAGGGTGGGTCCCCACTT
ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC
GTGTGGTATTGTACCCCGTCTCAGGTGTGGTCCAGTGTATTGCTTCACCCCGAGCC
CTGTTGTGGTGGGACGACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGCGAA
CGACTCGGATGTGCTGATTCTCAACAAACACGCGGCCGCCGAGGCAACTGGTTCGGC
TGTACATGGATGAATGGCACTGGGTTACCAAGACGTGTGGGGCCCCCGTGCAACA
TCGGGGGGCCGGCAACAAACACCTTGACCTGCCACTGACTGTTTCCGAAGCACCC
CGAGGCCACCTACGCCAGATCGGTTCTGGCCCTGGCTGACACCTAGGTGTGGTT
CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTACCATCTTAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGATGCAATTGGACTCG
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TCTACAACAGGTGATCGAGGGCAGACACCACCACTACCAACTAAATAG

SEQ ID NO 41 (HCCI43)

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CTTAGCCCCGGGCGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCAAACAGGGTTCTTGCCGAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTGGCCAGCTGCG
CTCCATCGACAAGTTCGCTCAGGGTGGGTCCCCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCCTACTGCTGGCACTACGCCCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGGTCCAGTGTATTGCTTCACCCCGAGGCCCTGGTGTGGTGGGAC
GACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGGGAACGACTCGGATGTGCTG
ATTCTCAACAAACACGCCGCCGCCGAGGCAACTGGTTGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGCCCCCGTGCAACATCGGGGGGCCGGCA
ACAACACCTTGACCTGCCCACTGACTGTTTCCGAAGCACCCCGAGGCCACCTACGC
CAGATCGGTTCTGGCCCTGGCTGACACCTAGGTGTATGGTTATTACCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTCAAGGTTAGGATGTACGTGGG
GGCGTGGAGCACAGGTTCGAAGCCGATGCAATTGGACTCGAGGAGAGCGTTGTGA
CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTACAACAGAGTGG
CAGAGCTTAATTAATTAG

Fig. 21I

SEQ ID NO 43 (HCCI44)

ATGGTGGGAACTGGCTAAGGTTGGTGTGACTCTTGCCTCGACG
GGCATAACCGCGTGTCAAGGAGGGCAGCAGCCTCGATACCAGGGCCTGTGTCCT
CTTAGCCCCGGGCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC
ATCAACAGGACTGCCCTGAACGACTCCCTCAAACAGGGTCTTGCCGAC
TATTCTACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCAGCTGCG
CTCCATCGACAAGTCGCTCAGGGTGGGTCCTCACTTACACTGAGCCTAACAGC
TCGGACCAGAGGCCACTGCTGGCACTACGCGCTCGACCGTGTGGTATTGTACCCG
CGTCTCAGGTGTGGTCCAGTGTATTGCTTACCCCGAGCCCTGTGTGGTGGGAC
GACCGATCGGTTGGTGTCCCCACGTATAACTGGGGGCGAACGACTCGGATGTGCTG
ATTCTCAACAAACACGCCCGCCCGAGGCAACTGGTTGGCTGTACATGGATGAATG
GCACTGGGTTACCAAGACGTGTGGGGCCCCCGTCAACATGGGGGGCCGGCA
ACAACACCTTGACCTGCCCCACTGACTGTTTGGAAAGCACCCCGAGGCCACCTACGC
CAGATGCGGTTCTGGGCTGGTGAACACCTAGGTGTATGGTCATTACCCATATAGG
CTCTGGCACTACCCCTGCACTGTCAACTTACCATCTTCAAGGTTAGGATGTACGTGG
GGCGTGGAGCACAGGTCGAAGCCGATGCAATTGGACTCGAGGAGAGCGTTGTGA
CTTGGAGGACAGGGATAGATCAGAGCTAGGGCTGCTGTCTACAACACAGGTGAT
CGAGGGCAGACACCATCACCAACATCACTAATAG

SEQ ID NO 45 (HCCL64)

ATGGTGGCGGGGGCCCATTGGGAGTCCTGGCGGGCTCGCTACTATTCCATGGTGG
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CCCAGGTGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAAC
AGGACTGCCCTGAACGACTCCCTCAAACAGGGTCTTGCCGACTATTCT
ACAAACACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCAGCTGCGCTCCAT
CGACAAGTTGCTCAGGGTGGGCTCCACTTACACTGAGCCTAACAGCTCGGAC
CAGAGGCCACTGCTGGCACTACGCGCTCGACCGTGTGGTATTGTACCCCGTCTC
AGGTGTGGTCCAGTGTATTGCTTACCCCGAGCCCTGTGTGGTGGGACGACCGA
TCGGTTGGTGTCCCCACGTATAACTGGGGGCGAACGACTCGGATGTGCTGATTCTC
AACAAACACGCCCGCCCGAGGCAACTGGTTGGCTGTACATGGATGAATGGCACT
GGGTTACCAAGACGTGTGGGGCCCCCGTCAACATGGGGGGCGGCAACAAAC
ACCTTGACCTGCCCCACTGACTGTTTGGAAAGCACCCCGAGGCCACCTACGCCAGAT
GGGTTCTGGGCCCCCTGGCTGACACCTAGGTGTATGGTCATTACCCATATAGGCTCTGG
CACTACCCCTGCACTGTCAACTTACCATCTTCAAGGTTAGGATGTACGTGGGGGCG

Fig. 21J

TGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAAGACGTTGTGACTTGGAG
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAACAGAGTCAGATA
CTGCCCTGTTCTTACCCACCCCTGCCGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTAGGGTCGGCGGTTGTCTCCCTTGTCA
ATCAAATGGGAGTATGTCCTGTTGCTCTCCTCCTGGCAGACGCGCGCATCTGCGC
CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGGCGCCTAGAGAACCTGGTG
GTCCTCAATGCCGCCGTGGCCGGGCGCATGGCACTCTTCCTCCTGTGTTCTT
CTGTGCTGCCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCAGCATACGCCCTAT
GGCGTGTGGCCGCTGCTCCTGCTGGCCTTACCACCACGAGCTATGCCTAGTAA

SEQ ID NO 47 (HCCI65)

AATTGGTAAGGTACGATACCCCTACATGGGCTTCGCCGACCTCGTGGGTACA
TTCCGCTCGCGGCCCGCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCG
GGTTCTGGAGGACGGCGTGAACATGCAACAGGGATTGCCCCGGTTGCTCTTCTCT
ATCTCCTCTGGCTTGTCTGACCGTTCCAGCTCCGCTTATGAAGTGCG
CAACGTGTCCGGATGTACCATGTCACGAACGACTGCTCCAACCTAACGATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCCTGCCCTGCCTGGAGAAC
AACTCTTCCCCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCAGTCGATTGCTCGTTGGGCGGCTGCTTCTG
TTCCGCTATGTACGTGGGGACCTCTGGGATCTGCTTCCTCGTCTCCAGCTGTTCA
CCATCTCGCCTGCCGGCATGAGACGGTGAGGACTGCAATTGCTCAATCTATCCGG
CCACATAACGGGTACCGTATGGCTGGGATATGATGATGAACTGGTCGCCTACAACG
GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGGACATGGTGGGG
GGGCCATTGGGAGTCCTGGCGGGCCTGCCTACTATTCCATGGTGGGAACTGGG
TAAGGTTTGGTTGTGATGCTACTCTTGCCTGGCGTCGACGGGACATACCCGCGTGT
GAGGGCAGCAGCCTCGATACCAGGGCCTTGTGCTCCCTTTAGCCCCGGTGGC
TCAGAAAATCCAGCTGAAACACCAACGGCAGTGGCACATCAACAGGACTGCCCT
GAAC TGCAACGACTCCCTCCAAACAGGGTTCTTGCCGCACTATTCTACAAACACAAA
TTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGCGCTCCATCGACAAGTTG
CTCAGGGTGGGTCCCTCACTTACACTGAGCCTAACAGCTCGGACCGAGGGCCTA
CTGCTGGCACTACGCGCTCGACCGTGTGGTATTGTACCCCGTCTCAGGTGTGG
CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGACGACCGATGGTTGG
CCCCACGTATAACTGGGGGGGAACGACTCGGATGTGCTGATTCTCAACAAACACGCG
CCGCCCGAGGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGTTACCAAGA
CGTGTGGGGCCCCCGTCAACATGGGGGGCCGGCAACAAACACCTTGACCTGCC

Fig. 21K

CCACTGACTTTTCGGAAGCACCCGAGGCCACCTACGCCAGATCGGGTCTGGGCC
CTGGCTGACACCTAGGTGTATGGTCATTACCCATATAAGGCTCTGGCACTACCCCTGCA
CTGTCAACTCACCATCTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGCACAGGTT
CGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTACTTGGAGGACAGGGATAG
ATCAGAGCTTAGCCCCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCCCTGTTCC
TTCACCACCCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAACATCGTGG
ACGTGCAATACTGTACGGTGTAGGGTGGCGTTGTCTCCCTGTCATCAAATGGGA
GTATGTCCTGTTGCTCTCCTCTGGCAGACCGCGCATCTGCGCCTGCTTATGGA
TGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTAGAGAACCTGGTGGTCCTCAATGC
GGCGGCCGTGGCCGGGGCGCATGGCACTCTTCCTCCTGTGTTCTCTGTGCTGCCT
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SEQ ID NO 49 (HCCI66)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCCAACCGCCGCCA
CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTGGTGGAGTTACCTGTTGCCGC
GCAGGGGCCCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCAAC
CTCGTGGAGGGCGACAACCTATCCCCAAGGCTGCCGACCCGAGGGTAGGGCCTGGG
CTCAGCCC GGTAACCTTGGCCCTCTATGGCAATGAGGGCATGGGTGGCAGGATG
GCTCCTGTCACCCCGCGGCTCTCGGCCTAGTTGGGCCCTACAGACCCCCGGCGTAGG
TCGCGTAATTGGTAAGGTATCGATACCCCTACATGCGGCTTCGCCGACCTCGTGG
GGTACATTCCGCTCGTGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG
CGTCCGGTTCTGGAGGGACGGCGTAACATGCAACAGGGATTGCCCAGGGTTGCTCT
TTCTCTATCTTCCCTTTGGCTTGCTGTCTGACCGTTCCAGCTCCGCTTATGAA
GTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACCAAGCATTG
TGTATGAGGCAGCGGACATGATCATGCACACCCCCGGTGCCTGCCGTTGGGA
GAACAACTCTCCCGCTGCTGGTAGCGCTACCCCCACGCTCGCAGCTAGGAACGCC
AGCGTCCCCACCAACGACAATACGACGCCACGTCGATTTGCTCGTGGGGCGGCTGCTT
TCTGTTCCGCTATGTACGTGGGGACCTCTCGGGATCTGTCTTCCCTCGTCTCCAGCTG
TTCACCATCTCGCCTGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC
CCGGCCACATAACGGGTACCGTATGGCTGGATATGATGATGAACTGGTGCCTAC
AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGT
GCGGGGGCCCATTGGGGAGTCCTGGCGGGCTCGCCTACTATTCCATGGTGGGGAACT
GGGCTAAGGTTTGGTTGTGATGCTACTCTTGCCGGCGTCACGGGCATAACCGCGT
GTCAGGAGGGCAGCAGCCTCCGATACCAAGGGCCTTGTGCTCCCTTTAGCCCCGGG

Fig. 21L

TCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT
GCCCTGAACGTCAACGACTCCCTCAAACAGGGTTCTTGCCGCACATTCTACAAAC
ACAAATTCAACTCGTCTGGATGCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAA
GTTCGCTCAGGGTGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG
CCCTACTGCTGGCACTACGCGCTCGACCGTGTGGTATTGTACCCCGTCTCAGGTGT
GCGGTCCAGTGTATTGCTTCACCCCCGAGCCCTGTTGGTGGGGACGACCGATCGGTT
TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC
ACGCGGCCGCGCGAGGCAACTGGTTGGCTGTACATGGATGAATGGCACTGGTTCA
CCAAGACGTGTGGGGCCCCCGTGCACACATCGGGGGGGCGCAACAAACACCTTGA
CCTGCCCCACTGACTGTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTT
TGGGCCCTGGCTGACACCTAGGTGTATGGTCATTACCCATATAGGCTCTGGCACTAC
CCCTGCACTGTCAACTCACCATCTCAAGGTTAGGATGTACGTGGGGGGCGTGGAGC
ACAGGTTCGAAGCCGATGCAATTGGACTCGAGGGAGAGCGTTGTGACTTGGAGGACA
GGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAAACAGAGTGGCAGATACTGCC
CTGTTCTTCACCACCCCTGCCGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC
ATCGTGGACGTGCAATACCTGTACGGTAGGGTGGCGGTTGTCTCCCTTGTCA
AATGGGAGTATGTCTGTTGCTCTTCTCCTGGCAGACGCGCGCATCTGCCCTGC
TTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCTTAGAGAACCTGGTGGTCC
TCAATGCCGGCGGCCGTGGCCGGGCCGATGGCACTCTTCCTTCTGTGTTCTGT
GCTGCCCTGGTACATCAAGGGCAGGCTGGCCCTGGCGGATACGCCCTATGGCG
TGTGGCCGCTGCTCTGCTTCTGCTGGCCTTACCAACCACGAGCTTATGCCTAGTAA

Fig. 22

OD measured at 450 nm
construct

Fraction	volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
START	23 ml	1/20	2.517	1.954	1.426	1.142
FLOW THROUGH	23 ml	1/20	0.087	0.085	0.176	0.120
1	0.4 ml	1/200	0.102	0.051	0.048	-0.050
2			0.396	0.550	0.090	0.067
3			2.627	2.603	2.481	2.372
4			3	2.967	3	2.694
5			3	2.810	2.640	2.154
6			2.694	2.499	1.359	1.561
7			2.408	2.481	0.347	1.390
8			2.176	1.970	1.624	0.865
9			1.461	1.422	0.887	0.604
10			1.236	0.926	0.543	0.519
11			0.981	0.781	0.294	0.294
12			0.812	0.650	0.249	0.199
13			0.573	0.432	0.239	0.209
14			0.653	0.371	0.145	0.184
15			0.441	0.348	0.151	0.151
16			0.321	0.374	0.098	0.106
17			0.525	0.186	0.099	0.108
18			0.351	0.171	0.083	0.090
19			0.192	0.164	0.084	0.087

Fig. 23

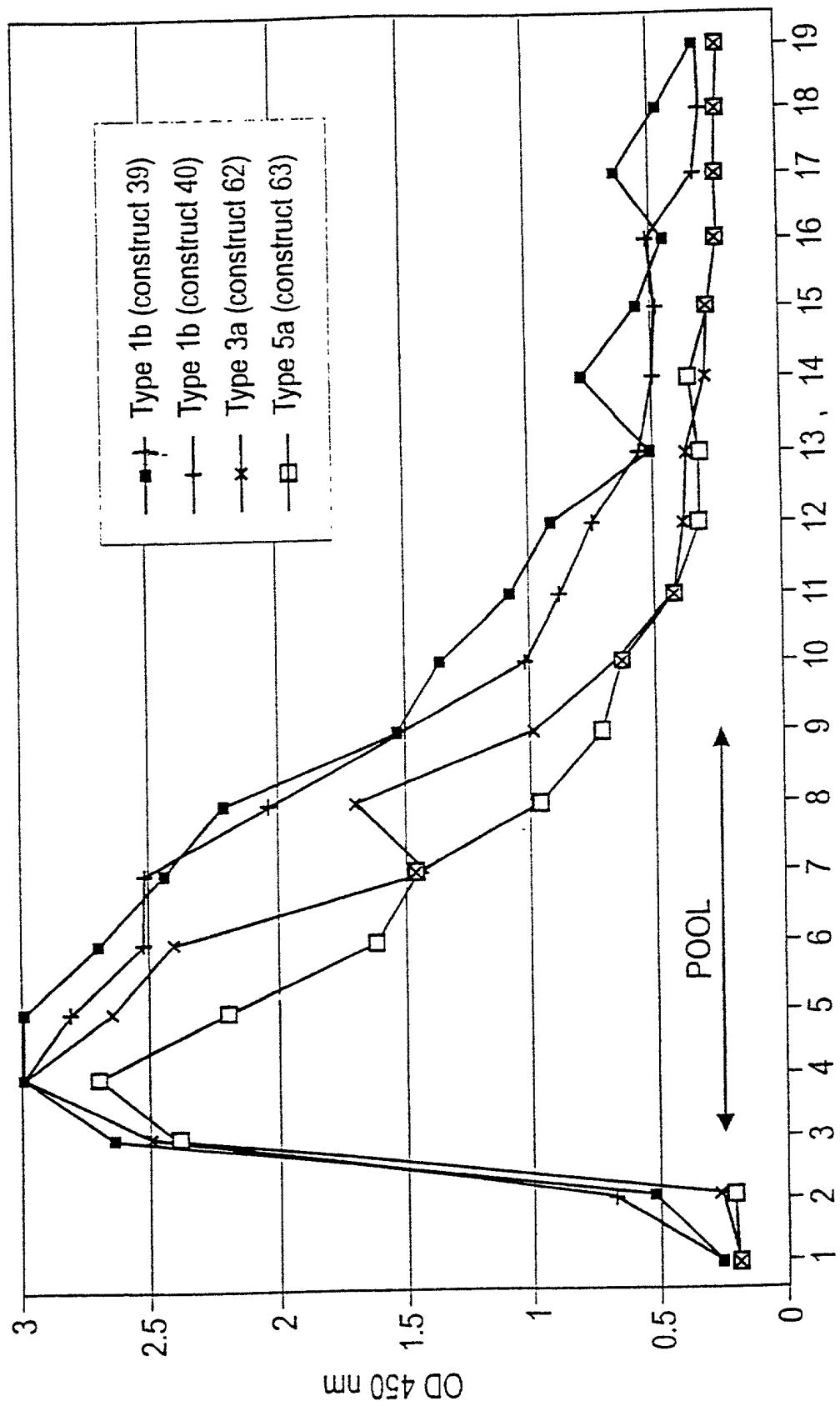


Figure 24

Fraction	volume	dilution	OD measured at 450 nm			
			construct			
			39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a
20	250 μ l	1/200	0.072	0.130	0.096	0.051
21			0.109	0.293	0.084	0.052
22			0.279	0.249	0.172	0.052
23			0.093	0.151	0.297	0.054
24			0.080	0.266	0.438	0.056
25			0.251	0.100	0.457	0.048
26			3	1.649	0.722	0.066
27			3	3	2.525	0.889
28			3	3	3	2.345
29			3	3	2.849	2.580
30			2.227	1.921	1.424	1.333
31			0.263	0.415	0.356	0.162
32			0.071	0.172	0.154	0.064
33			0.103	0.054	0.096	0.057
34			0.045	0.045	0.044	0.051
35			0.043	0.047	0.045	0.046
36			0.045	0.045	0.049	0.040
37			0.045	0.047	0.046	0.048
38			0.045	0.048	0.047	0.057
39			0.045	0.048	0.050	0.057
40			0.046	0.049	0.048	0.049

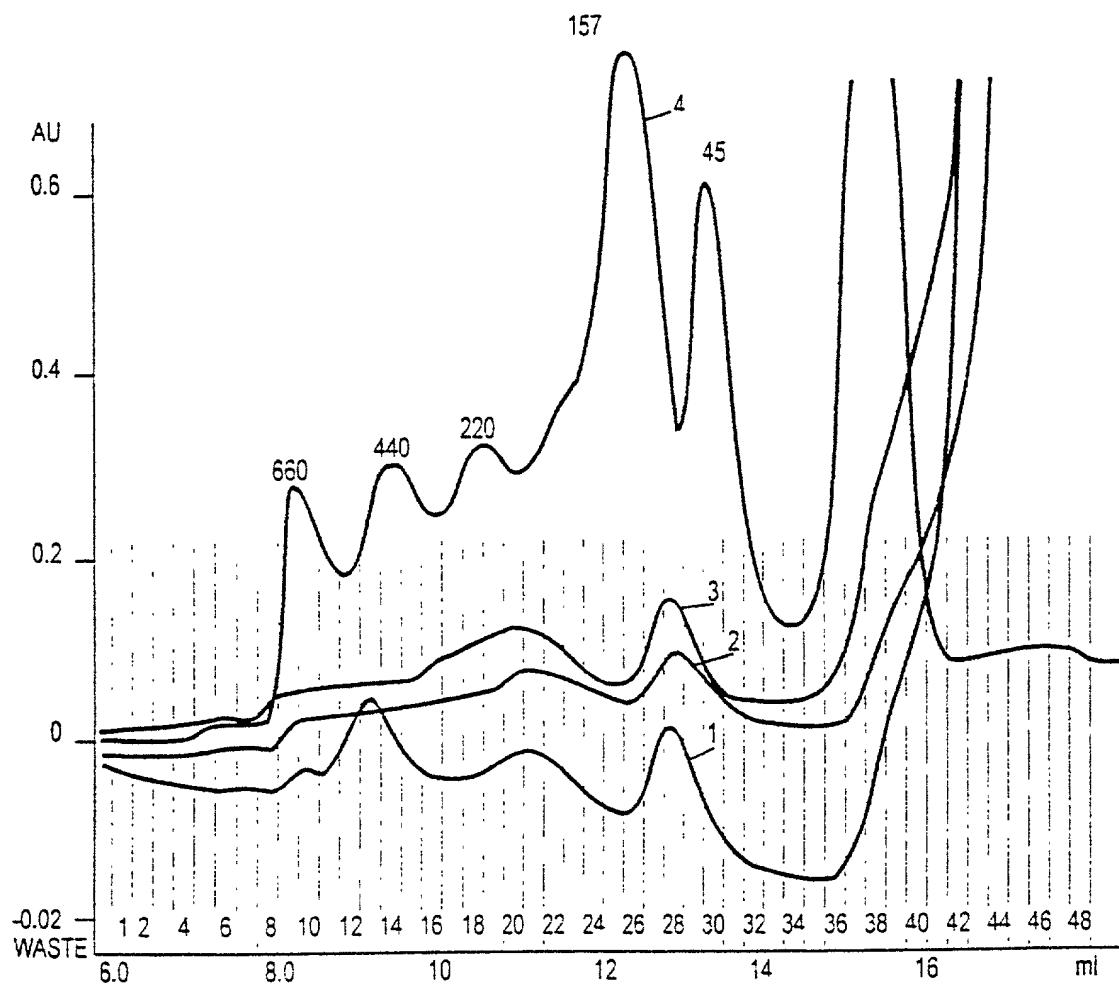


Fig. 25

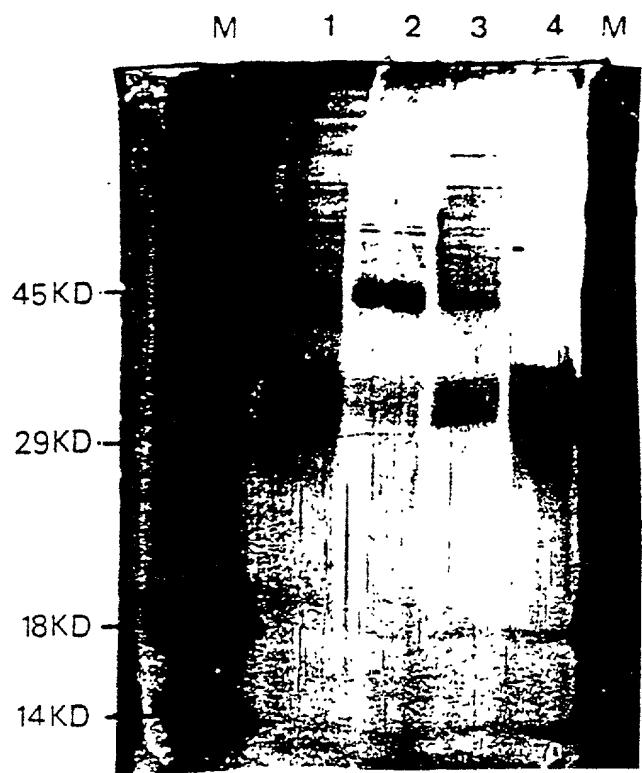


Fig. 26

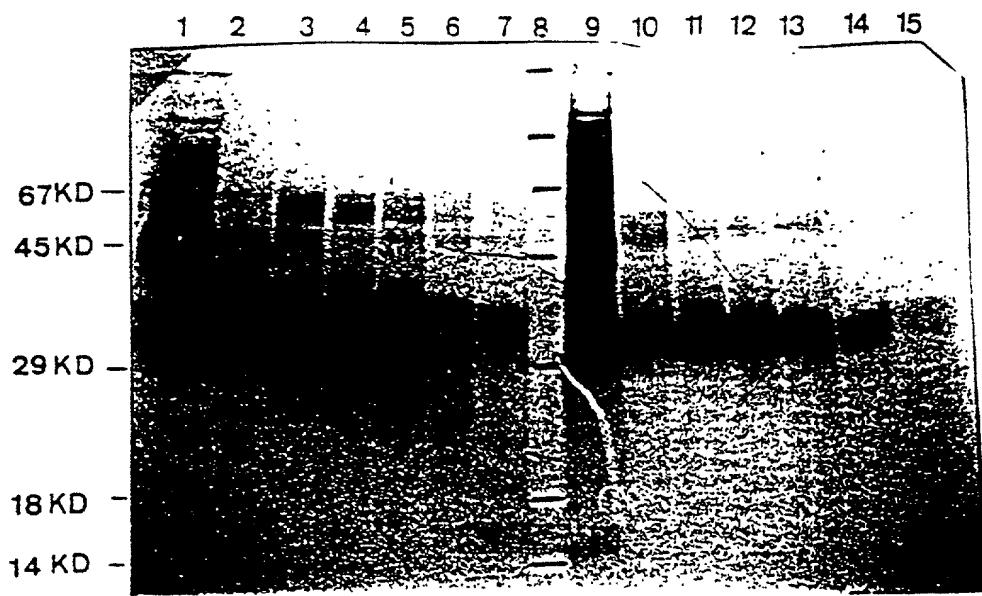


Fig. 27

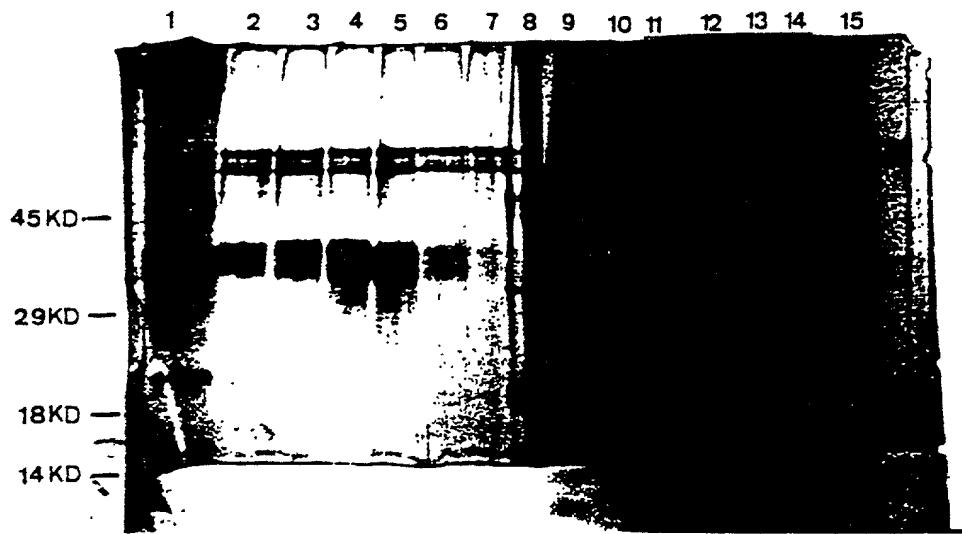


Fig.28

M 1 2 3 4 5 6

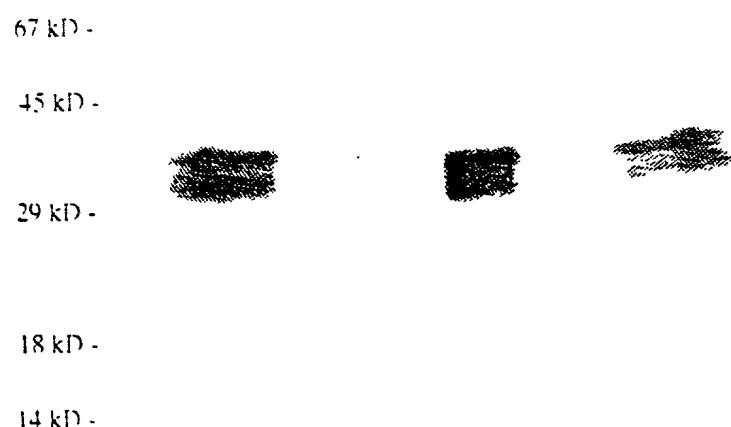


Fig.29

- Lane 1: Crude Lysate
- Lane 2: Flow through Lentil Chromatography
- Lane 3: Wash with EMPIGEN Lentil Chromatography
- Lane 4: Eluate Lentil Chromatography
- Lane 5: Flow through during concentration lentil eluate
- Lane 6: Pool of Elaster Size Exclusion Chromatography

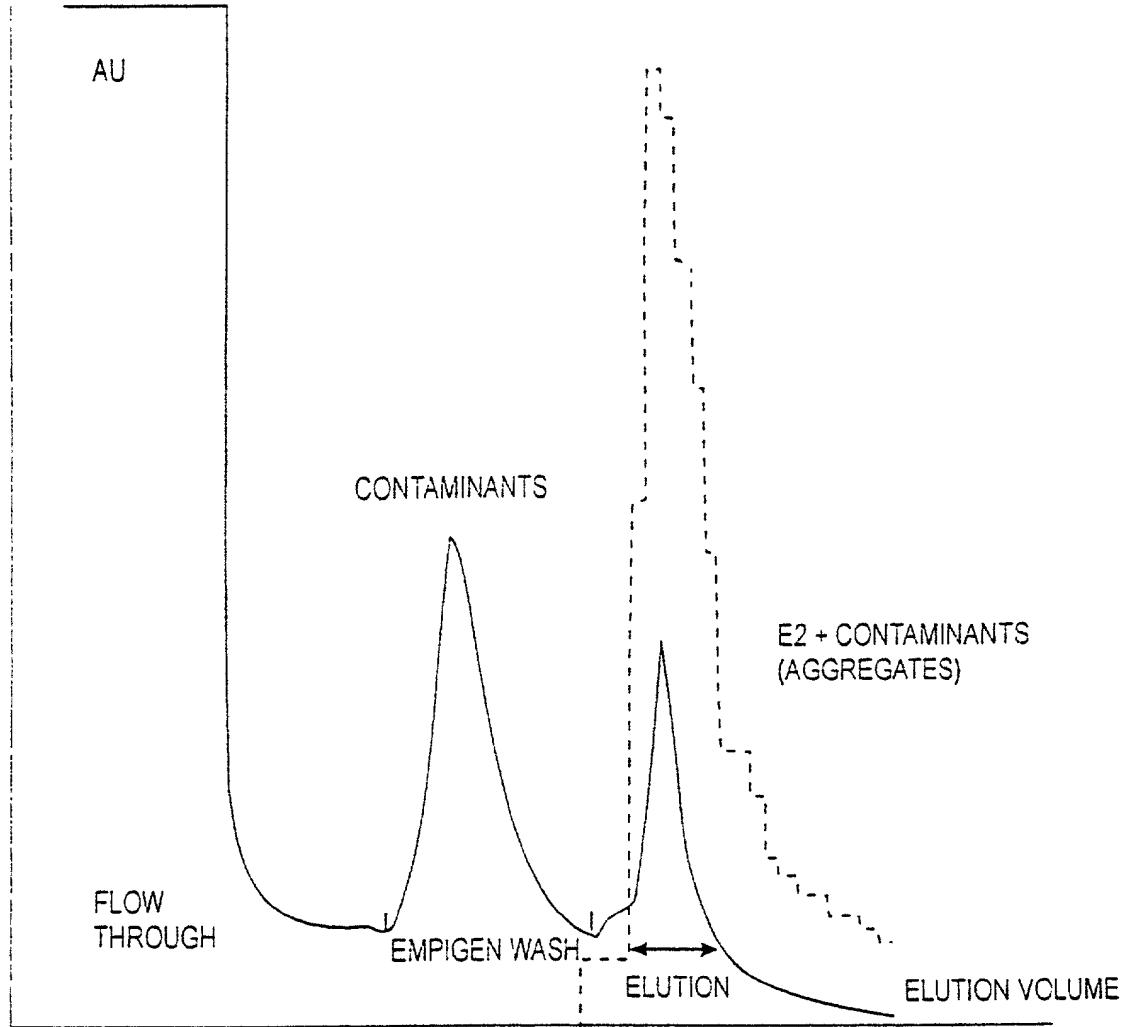
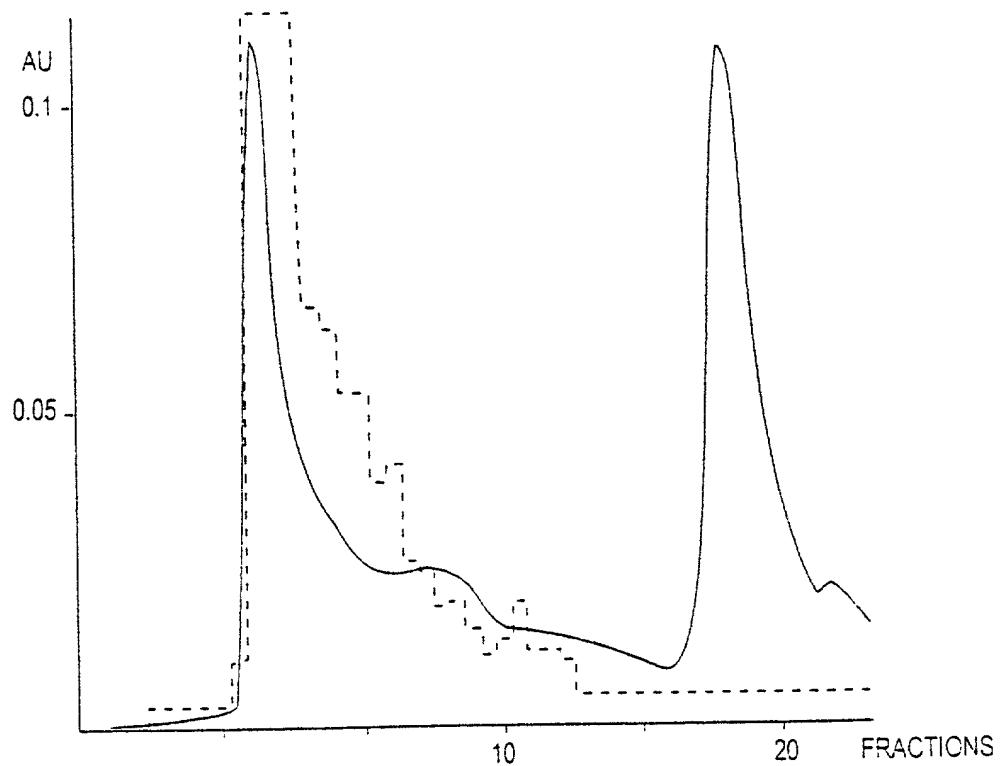


Fig. 30

NON - REDUCED

Fig. 31A

E2 + CONTAMINANTS (AGGREGATES)



REDUCED

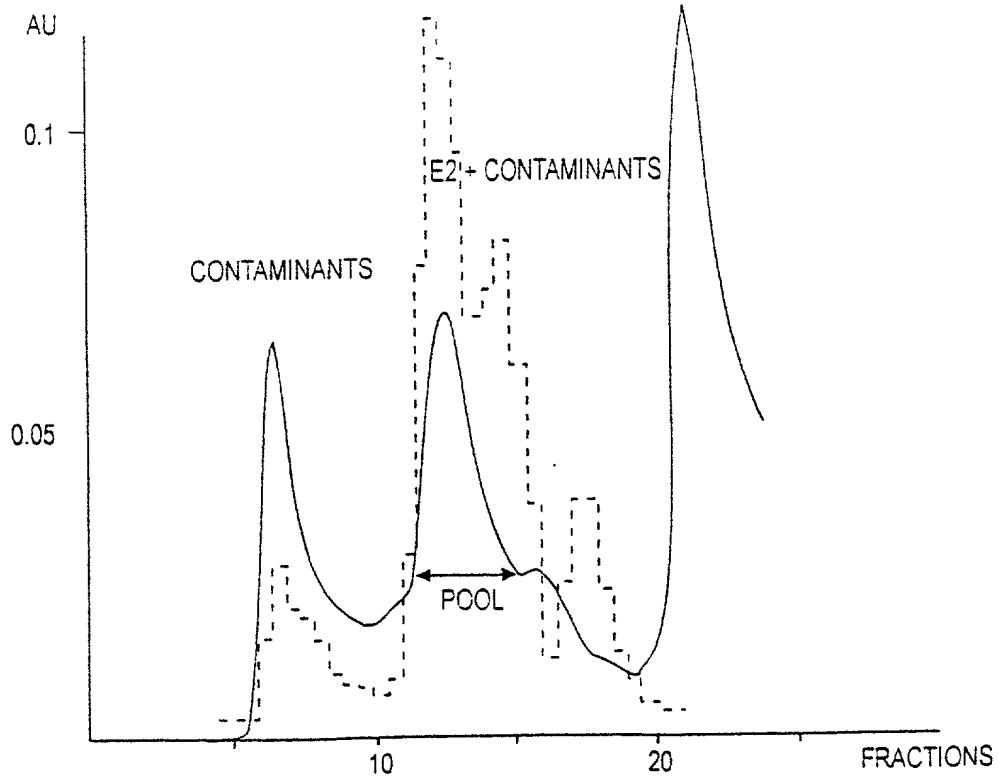


Fig. 31B

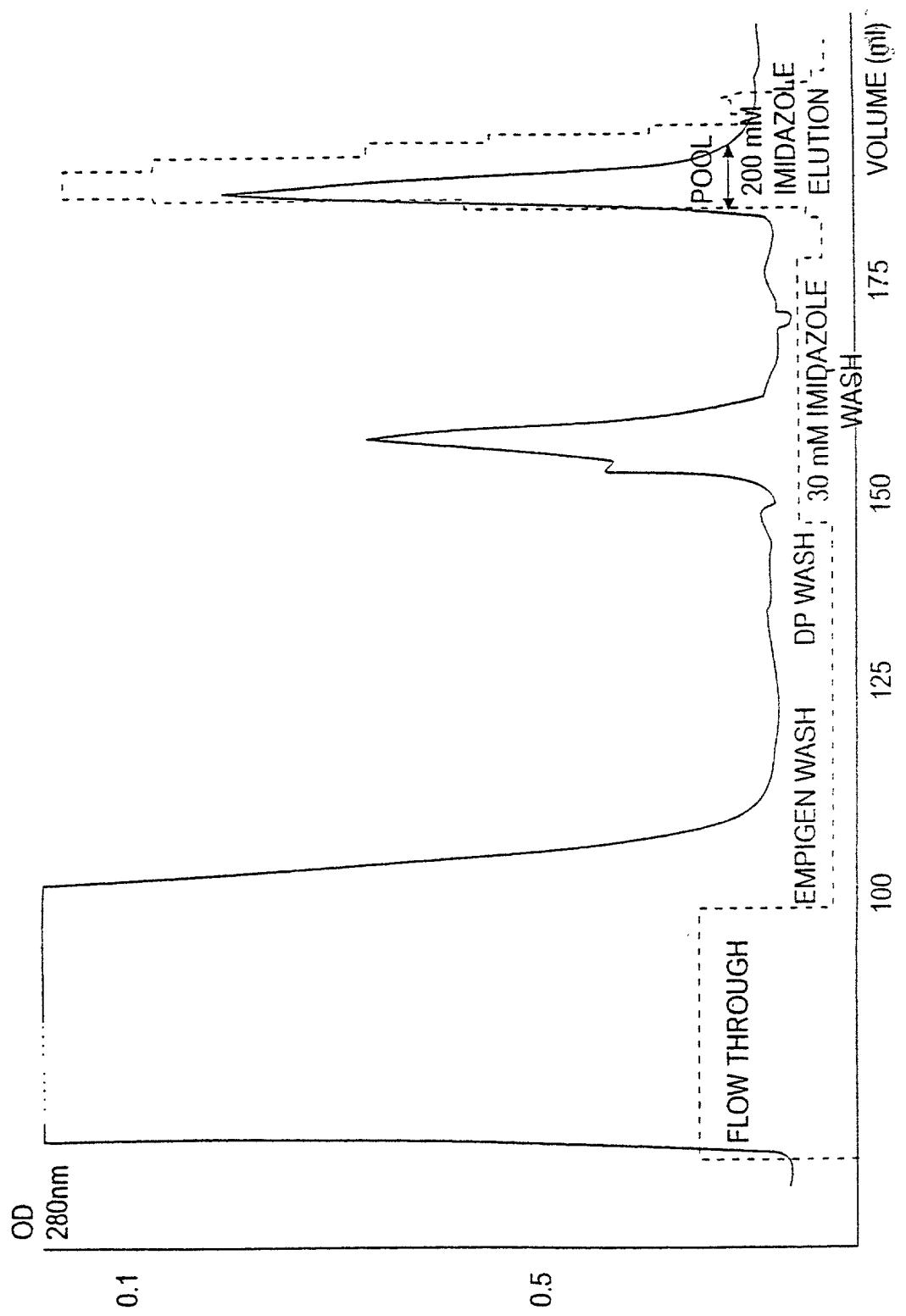
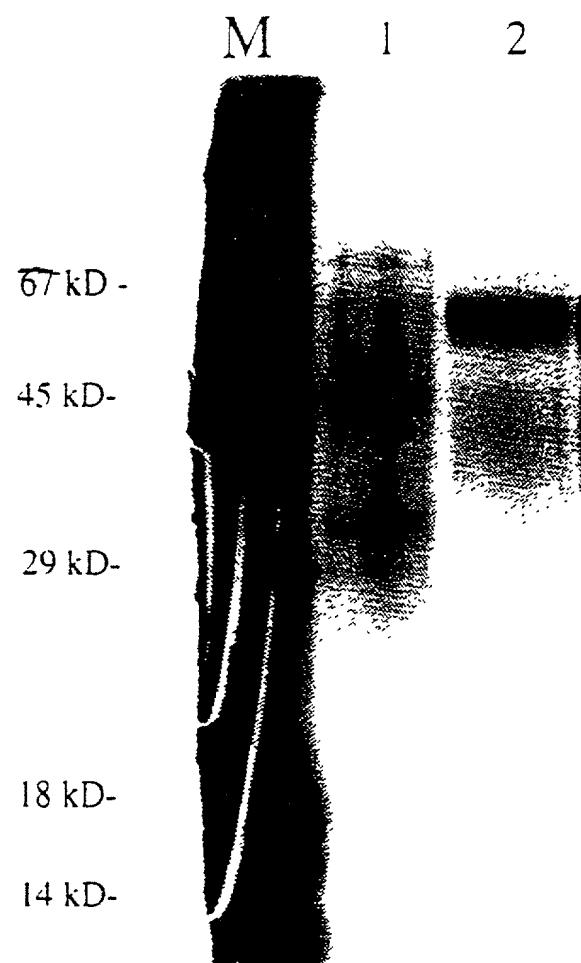


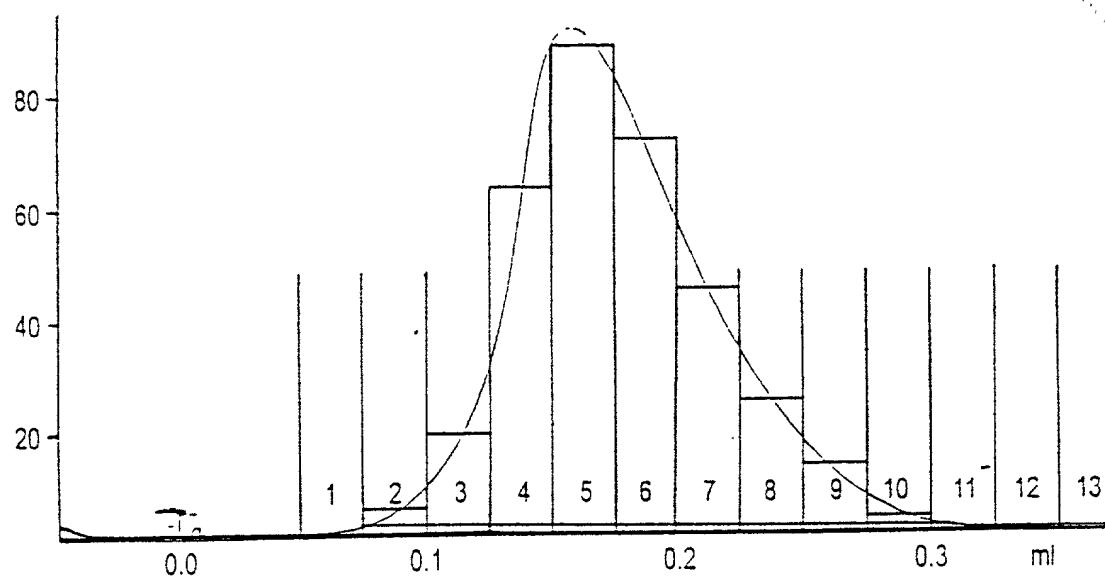
Fig. 32

SILVER STAIN OF PURIFIED E2



1. 30 mM IMIDAZOLE WASH Ni-IMAC
2. 0.5 ug E2

Fig. 33



No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4

Total Area above baseline = 0.796522 ml*AU

Total area in evaluated peaks = 0.796521 ml*AU

Ratio peak area / total area = 0.999999

Total peak duration = 2.613583 ml

Fig. 34

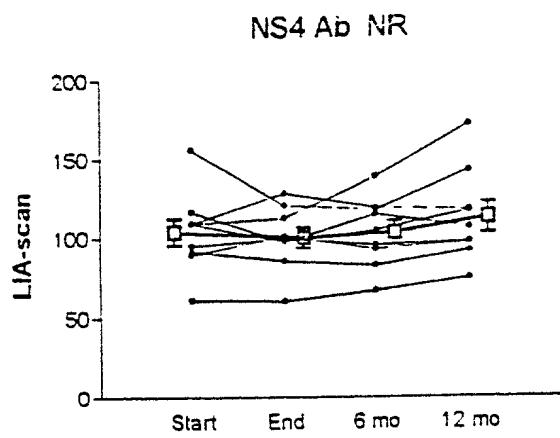


Fig. 35A-1

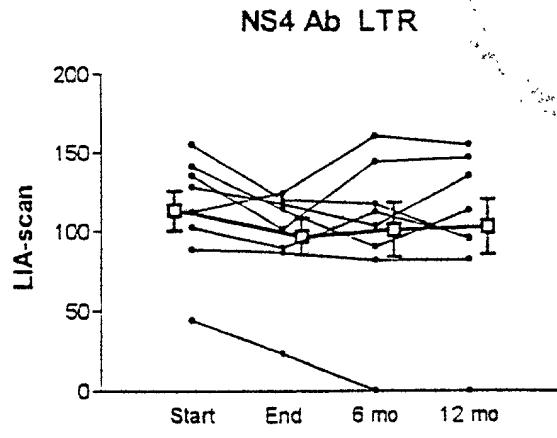


Fig. 35A-2

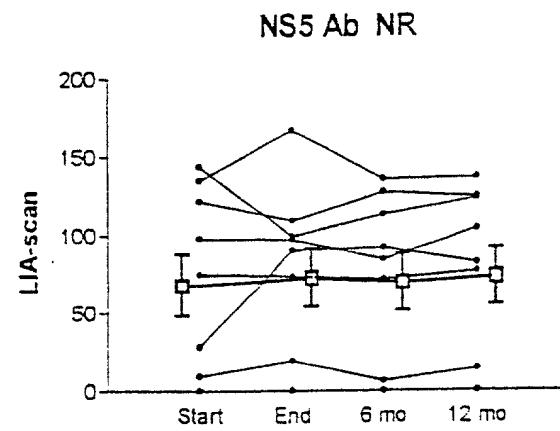


Fig. 35A-3

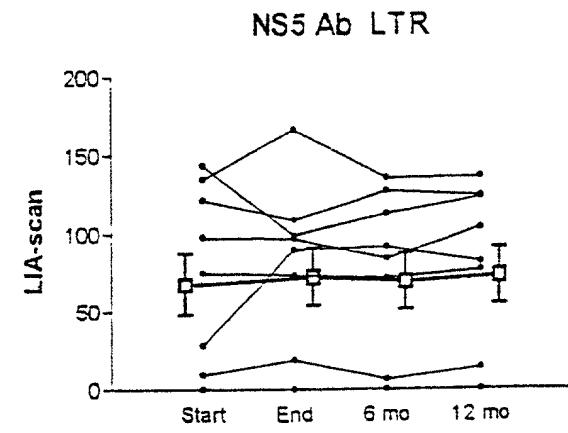


Fig. 35A-4

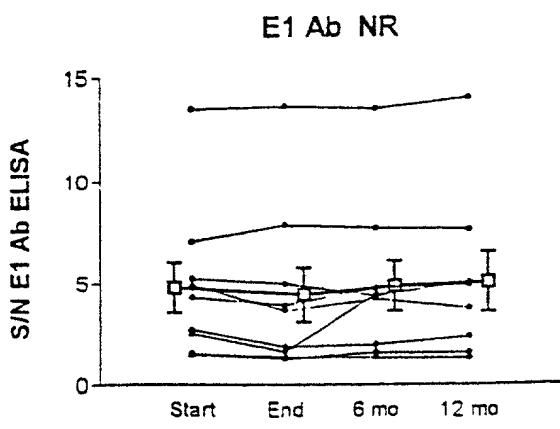


Fig. 35A-5

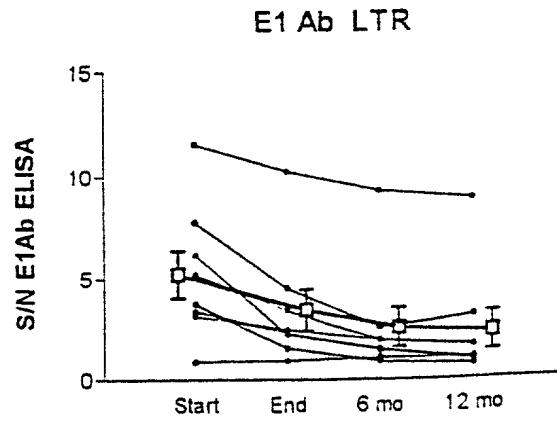


Fig. 35A-6

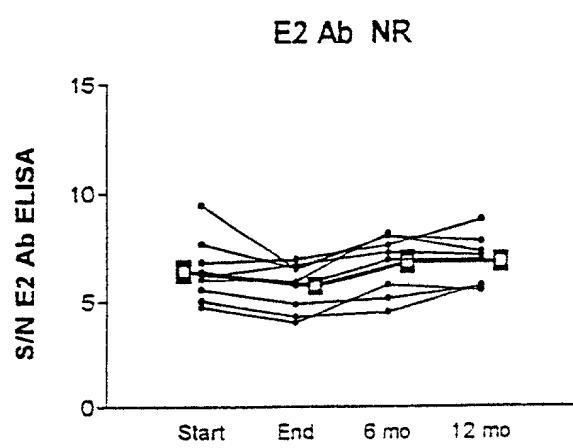


Fig. 35A-7

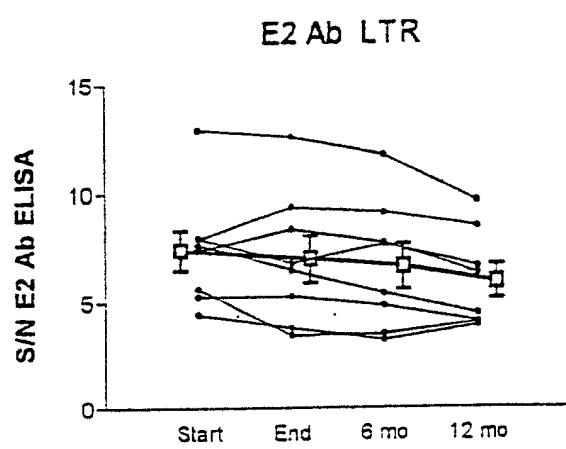


Fig. 35A-8

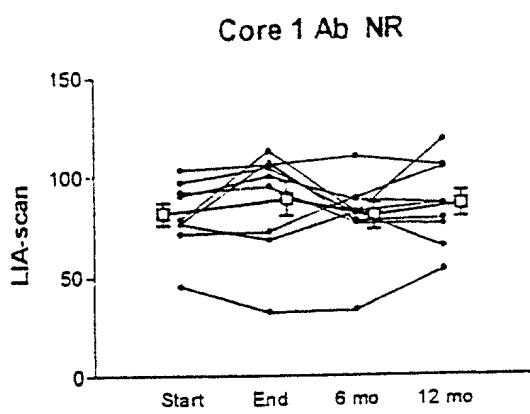


Fig. 35B-1

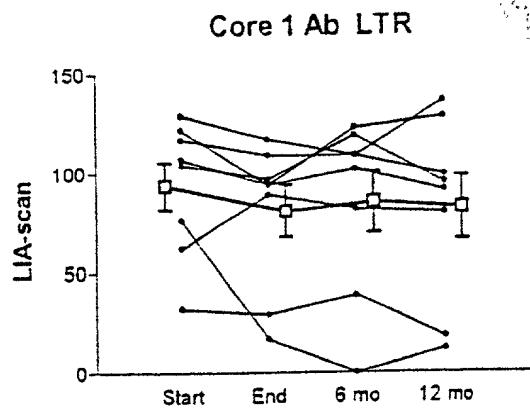


Fig. 35B-2

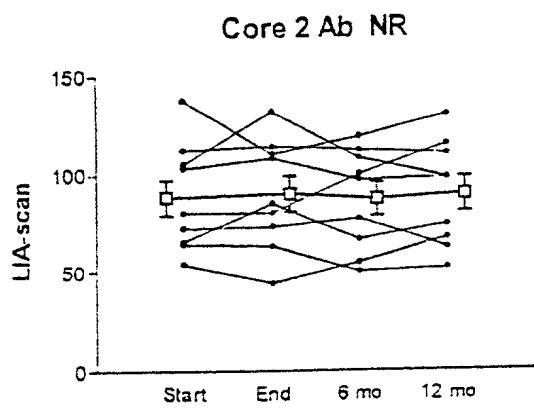


Fig. 35B-3

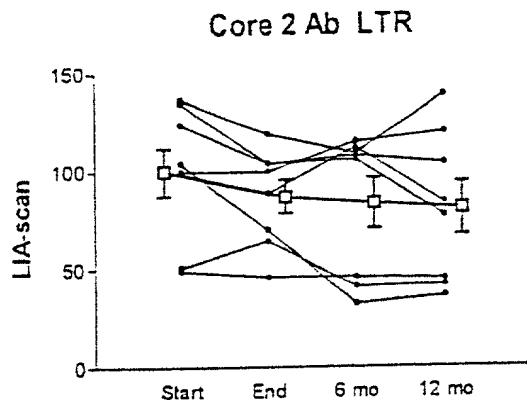


Fig. 35B-4

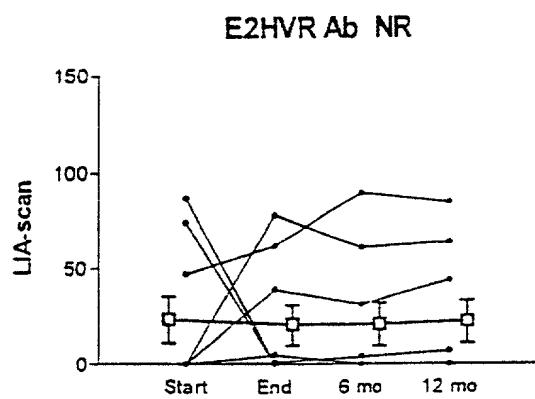


Fig. 35B-5

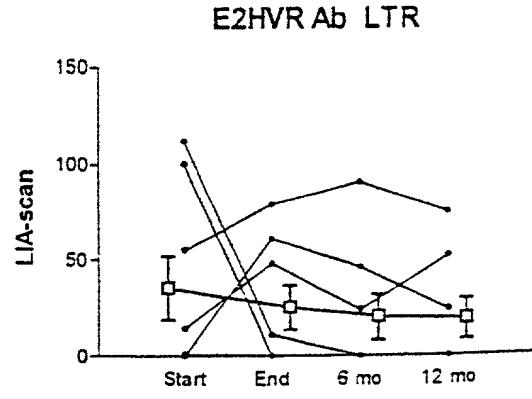


Fig. 35B-6

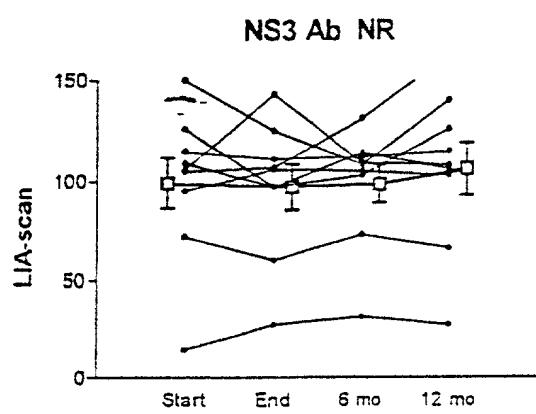


Fig. 35B-7

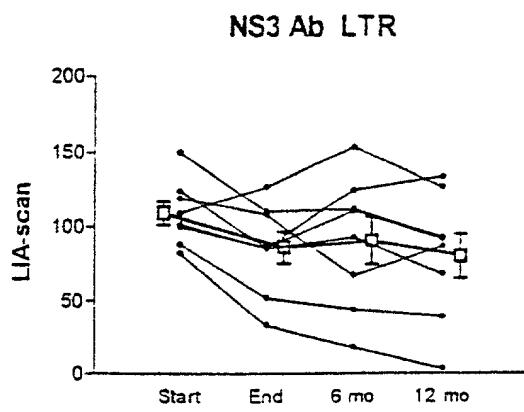


Fig. 35B-8

Fig. 36A

E1 Ab

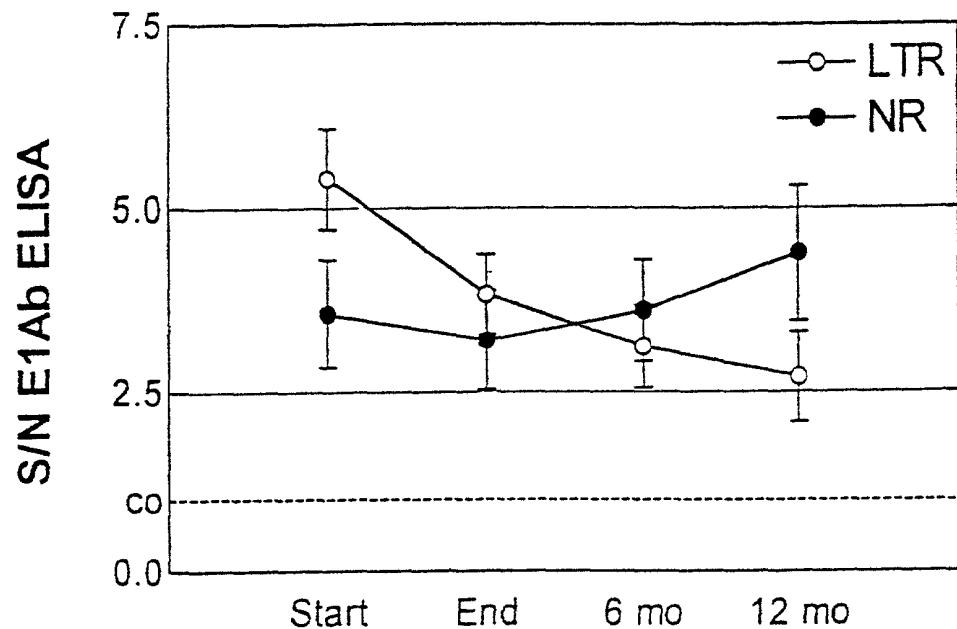


Fig. 36B

E2 Ab

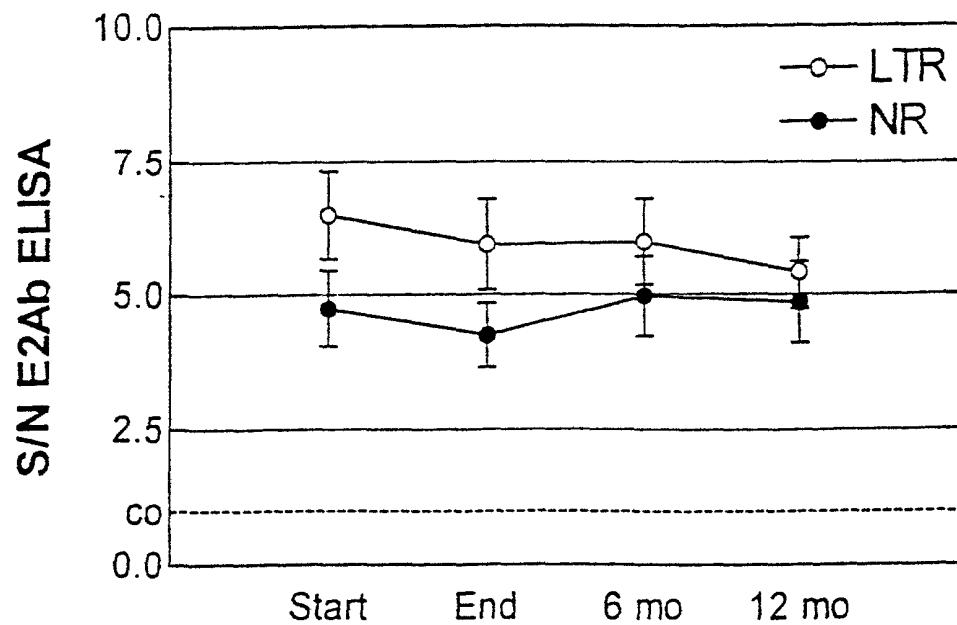


Fig. 37A
Non Responders

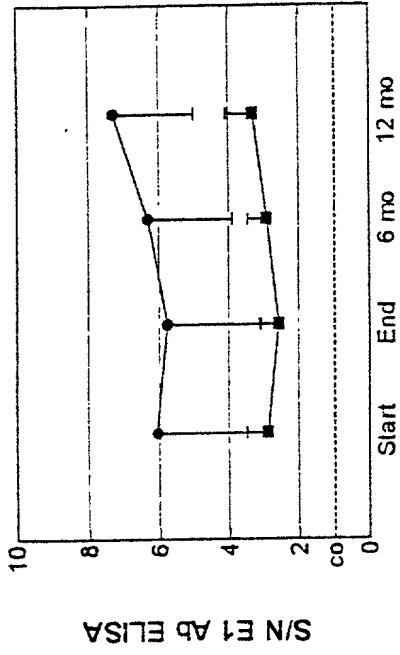


Fig. 37B
Long Term Responders

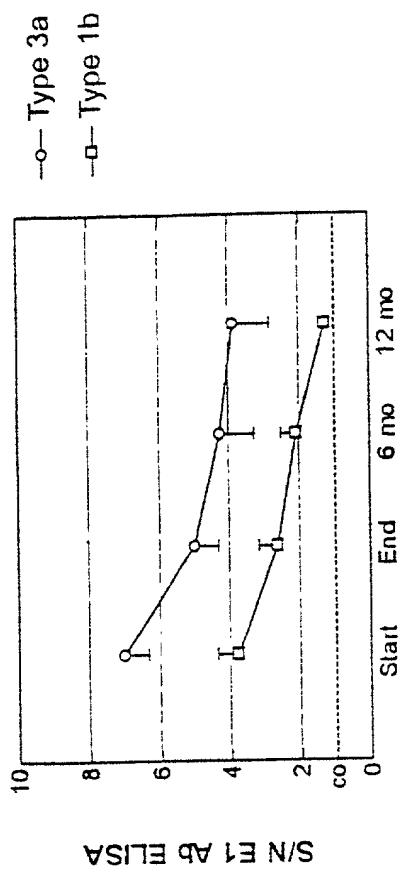


Fig. 37C
Type 1b

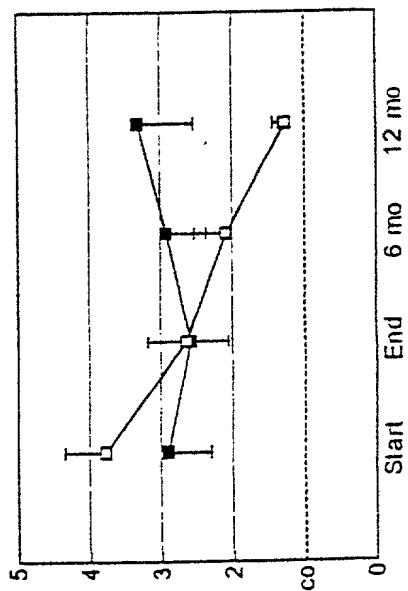


Fig. 37D
Type 3a

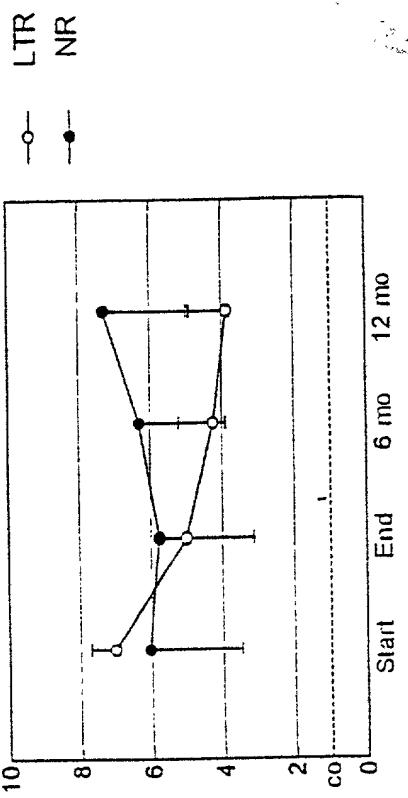
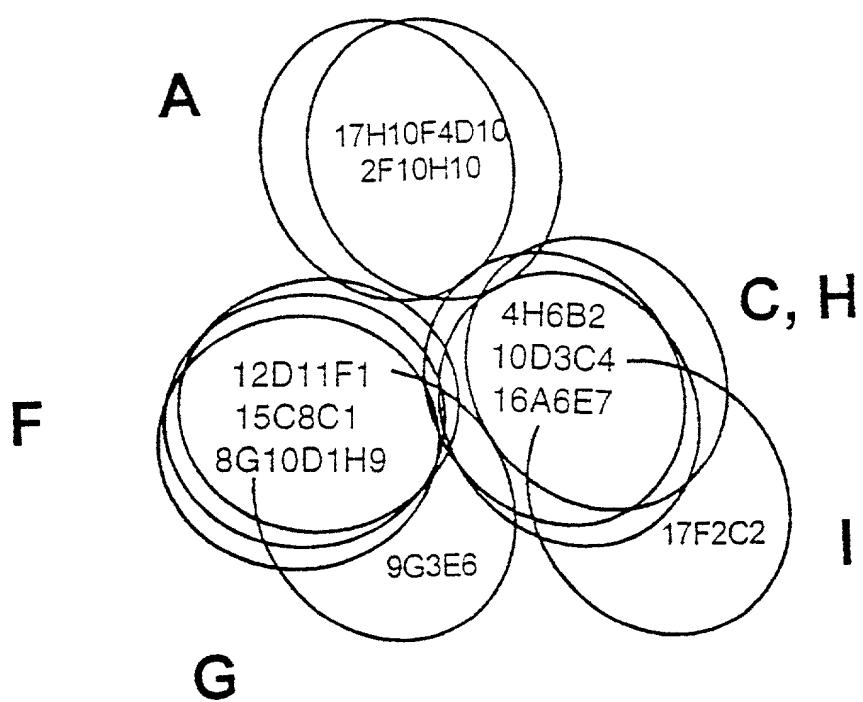


Fig. 38

Relative Map Positions of
anti-E2 monoclonal antibodies



PARTIAL DEGLYCOSYLATION
OF HCV E1 ENVELOPE PROTEIN

Endoglycosidase H
(Endo H) Glycopeptidase F
(PNGase F)

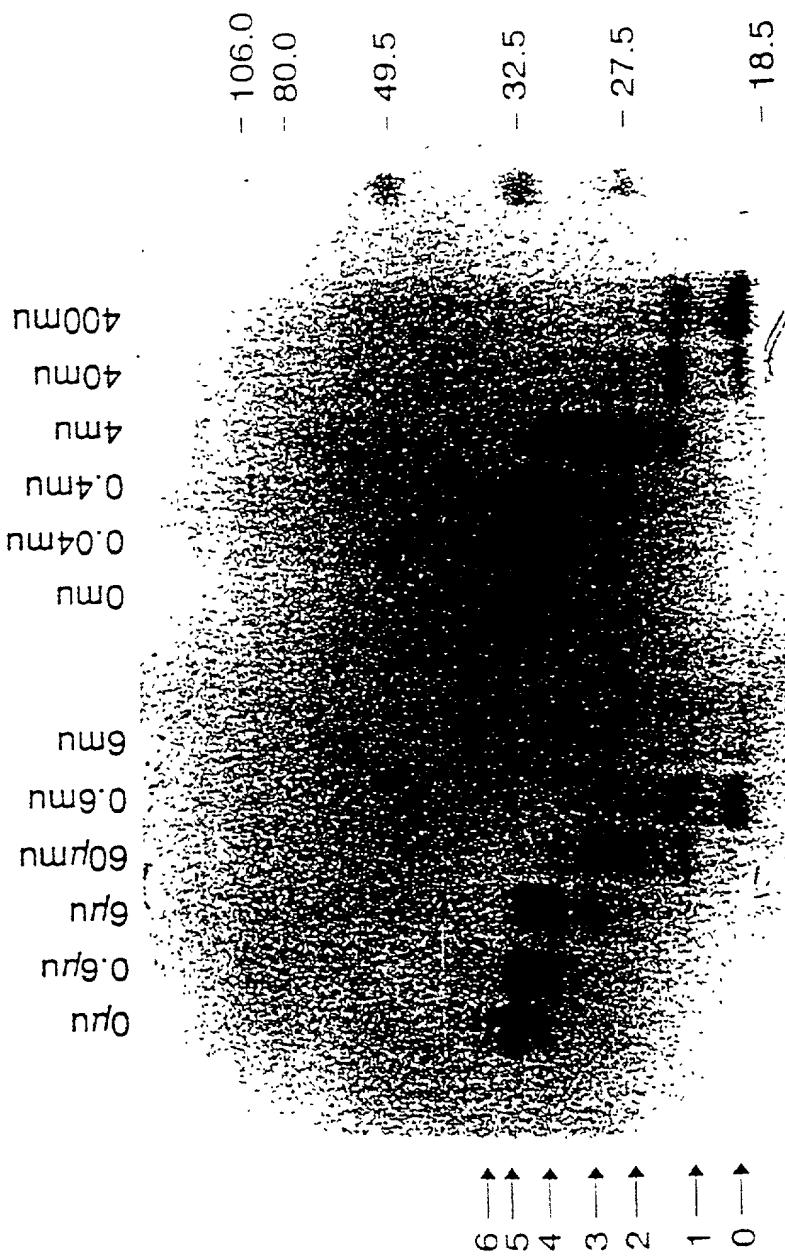


Fig.39

PARTIAL TREATMENT OF HCV E2\E2s ENVELOPE PROTEINS
BY PNGase F

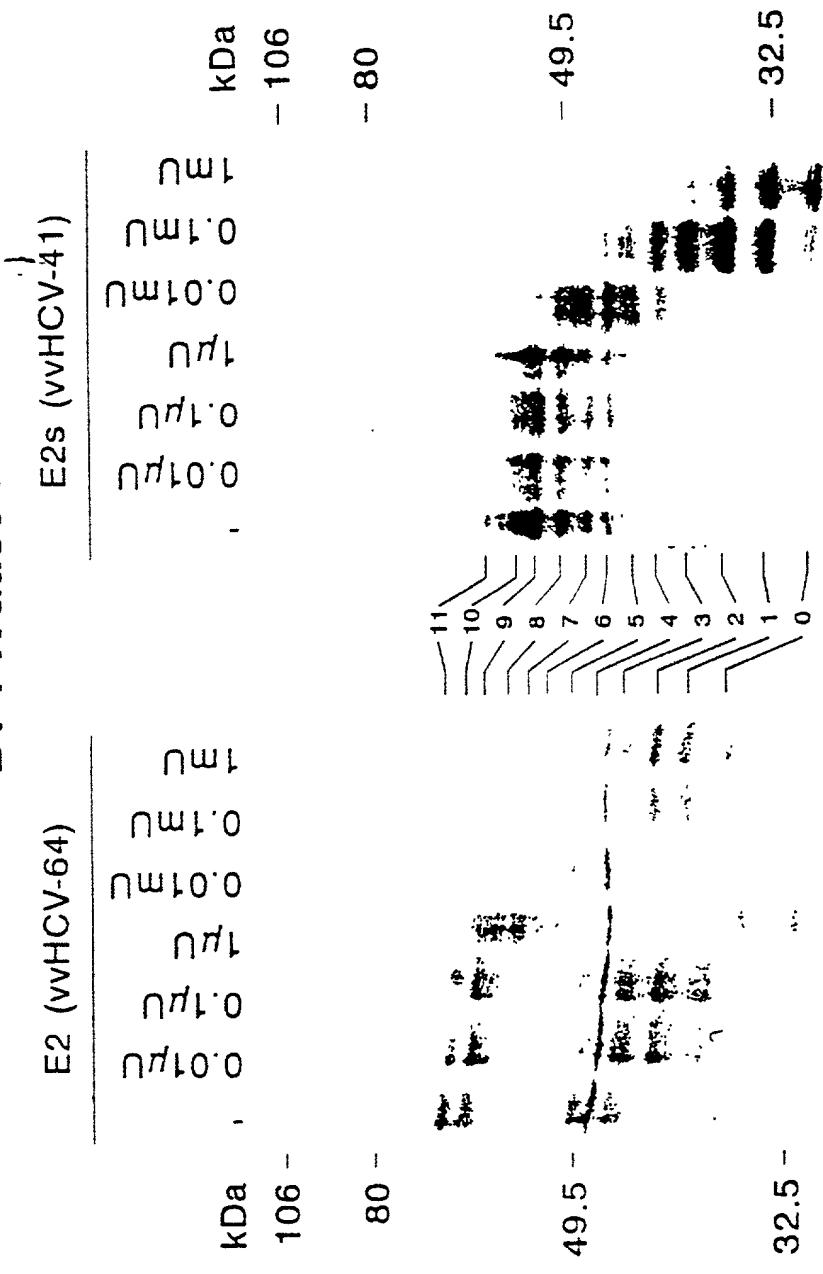


Fig. 40

Fig. 41 *In Vitro* Mutagenesis of HCV E1 glycoprotein

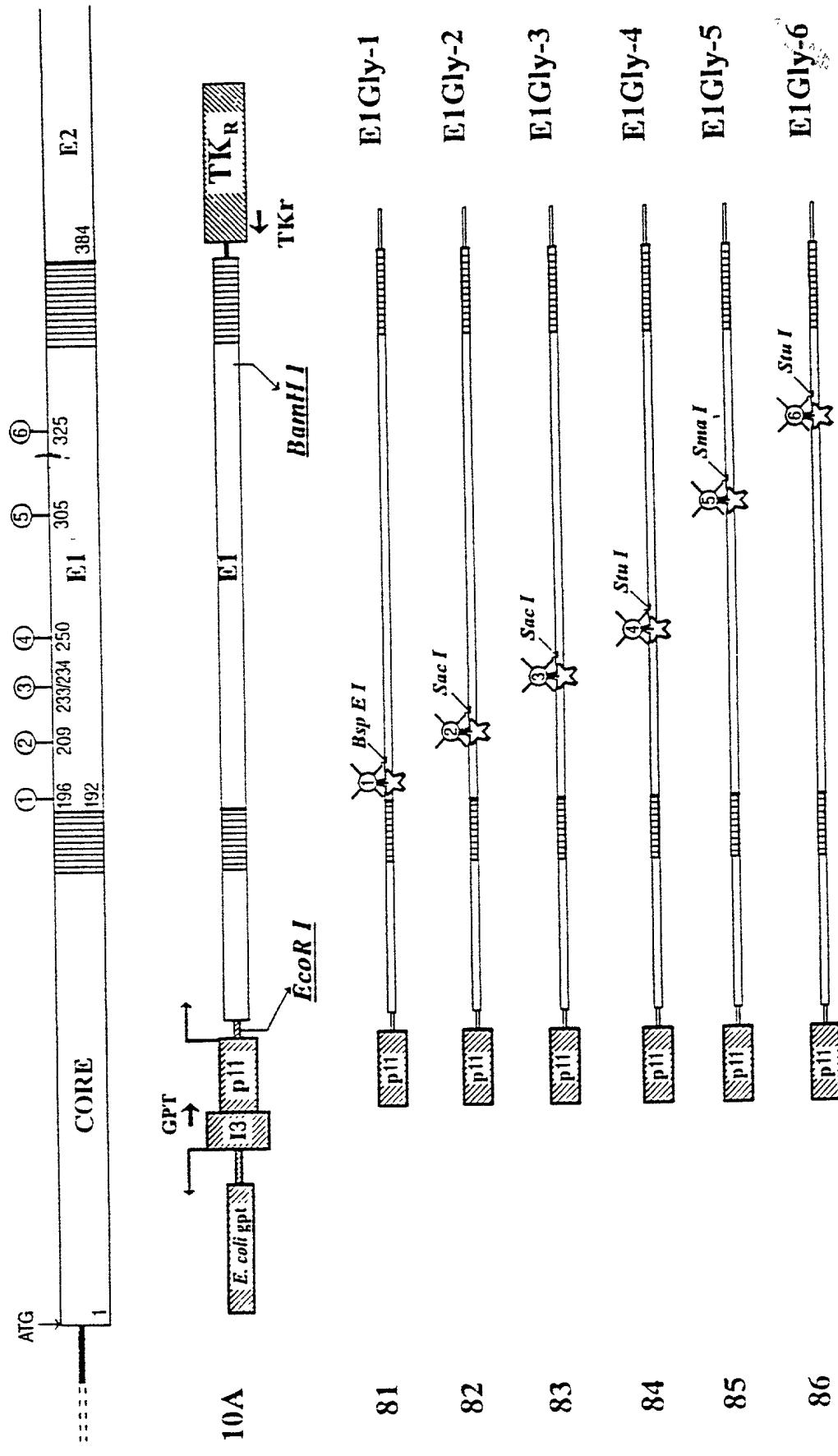
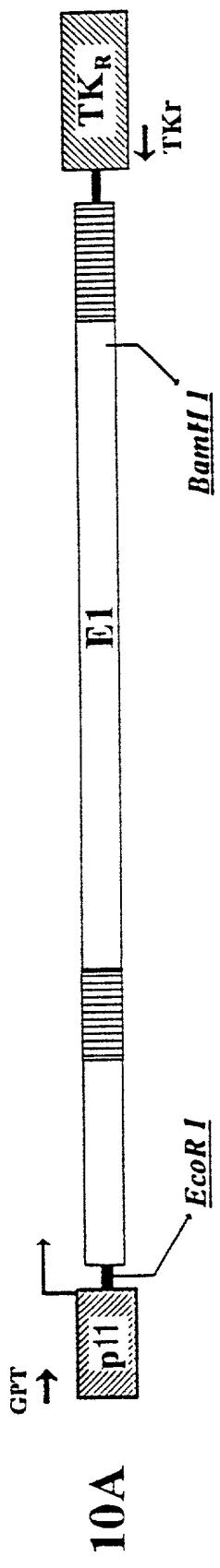
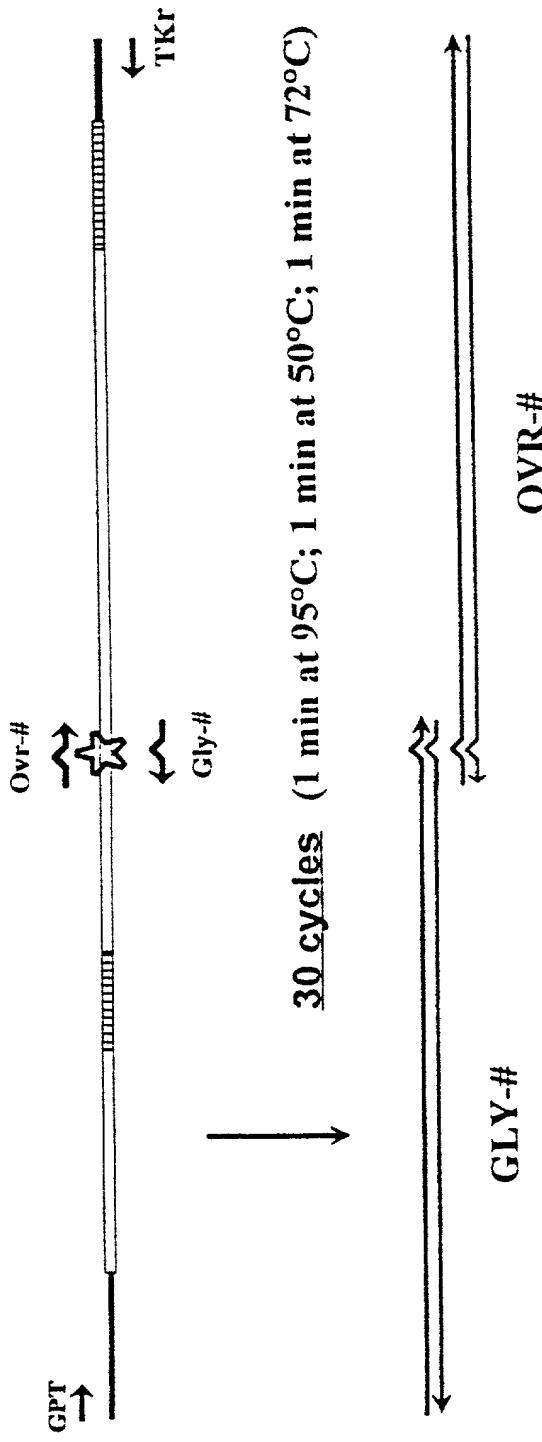


Fig. 42A *In Vitro* Mutagenesis of HCV E1 glycoprotein



1. First step of PCR amplification (Gly-# and Ovr-# primers)



2. Overlap extension and nested PCR

a. Overlap extension

Fig. 42B

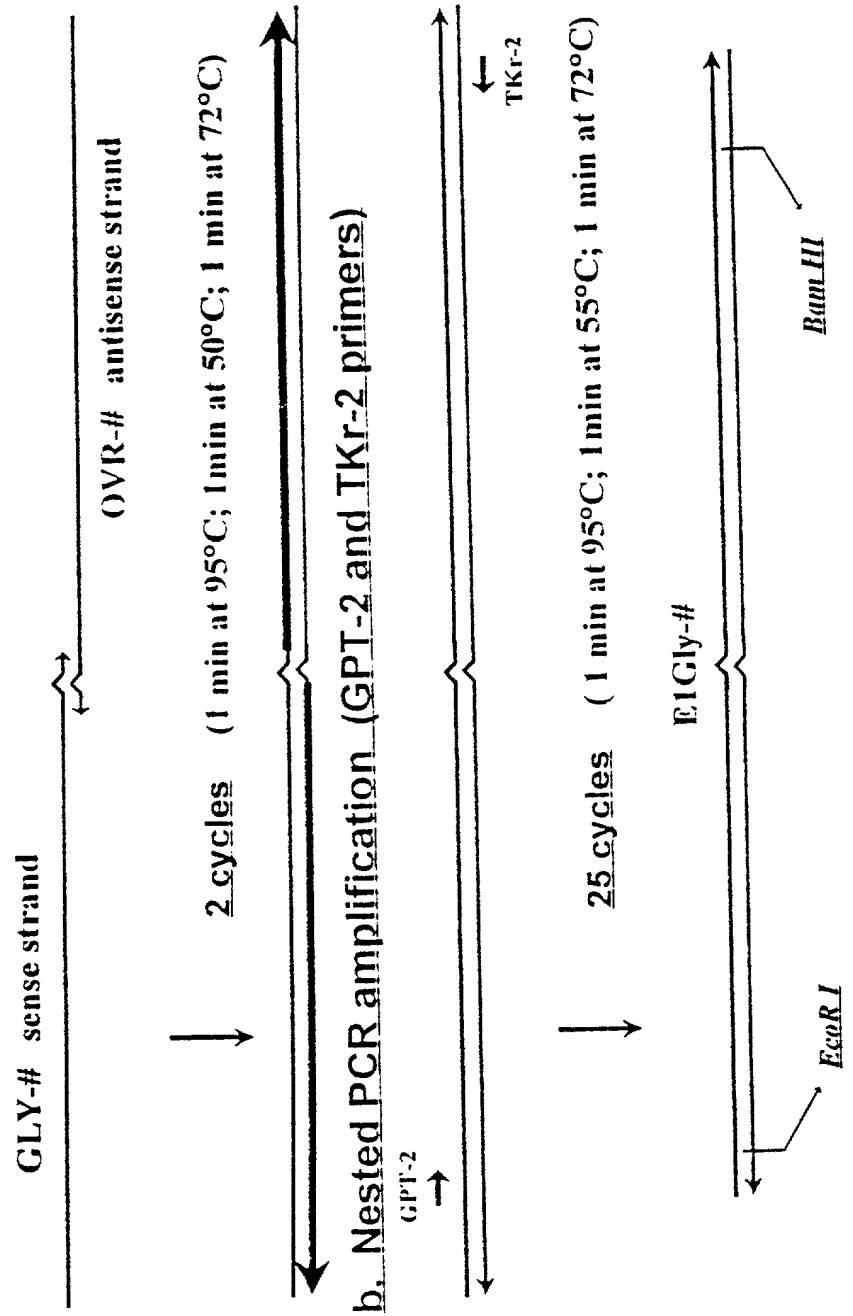
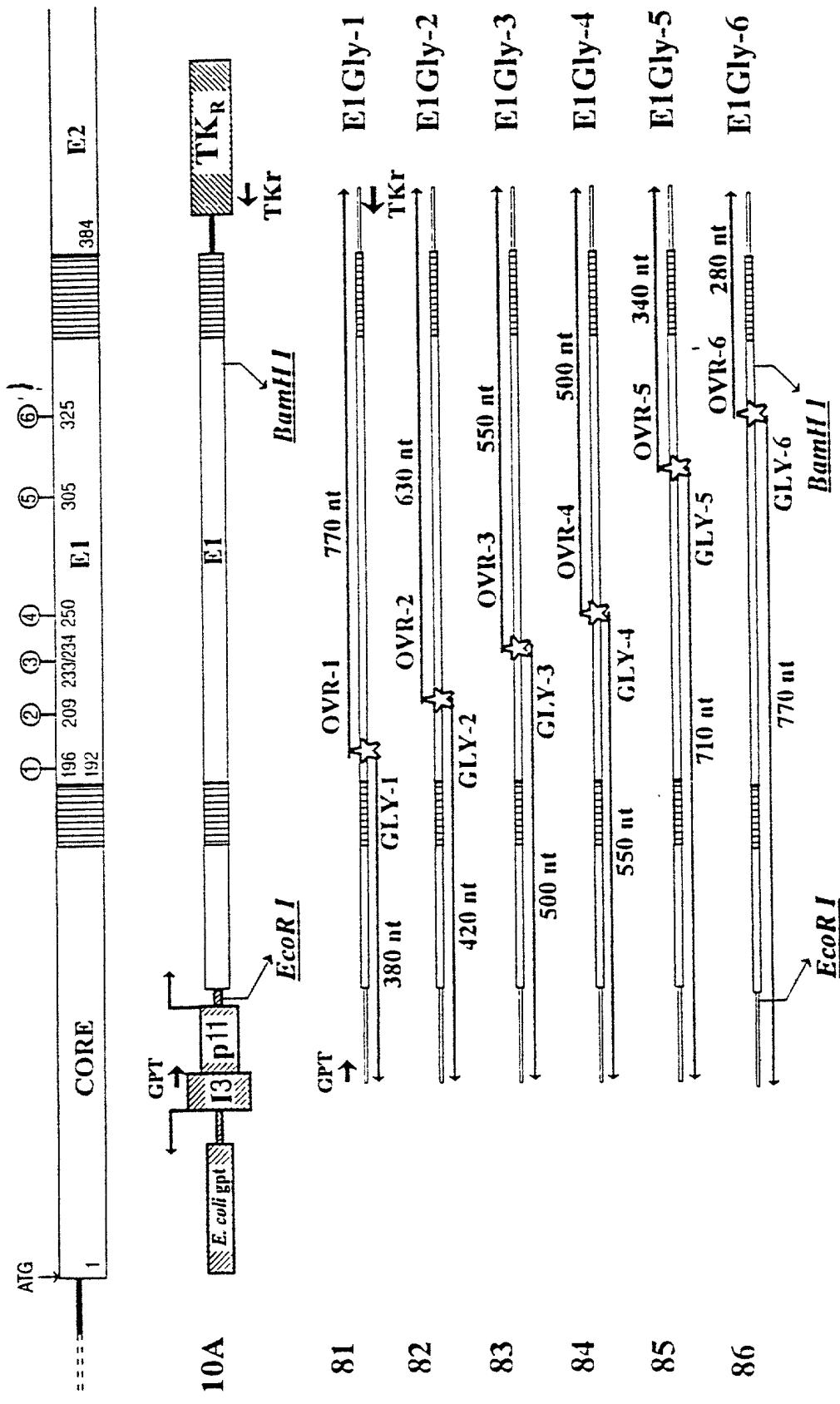


Fig. 43 *In Vitro* Mutagenesis of HCV E1 glycoprotein



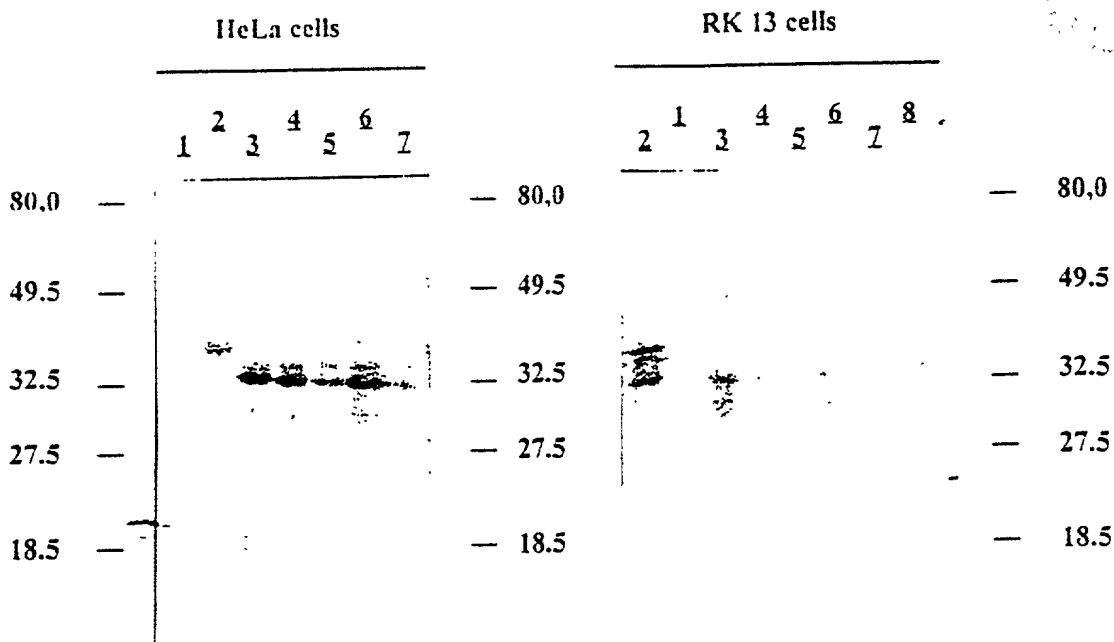


Fig. 44A

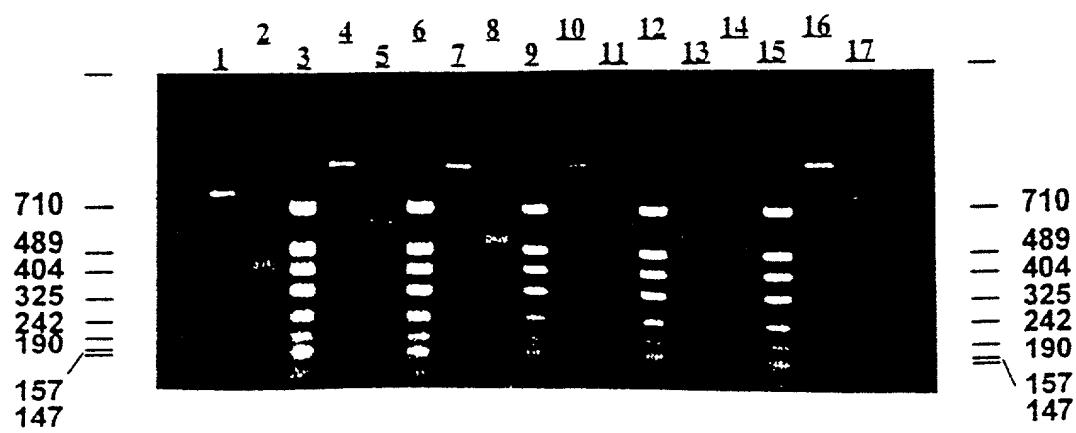


Fig. 44B

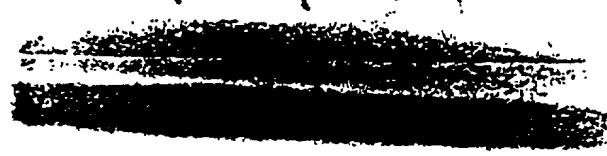


Fig.45

KDa 19 67 43 29 18



Fig.46